

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E

(ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE

(iii) NUMBER OF SEQUENCES: 183

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
(B) STREET: 600 South Avenue West
(C) CITY: Westfield
(D) STATE: New Jersey
(E) COUNTRY: U.S.A.
(F) ZIP: 07090

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word, Version 6.0c

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/509,359
(B) FILING DATE: 31-JUL-95
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Palisi, Thomas M.
(B) REGISTRATION NUMBER: 36629

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 654-5000
(B) TELEFAX: (908) 654-7866

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG

60

76

GAAGGAACCT	GAGCTACGAG	CCGCGGCGGC	AGCGGGGCGG	CGGGGNAAGC	GTATACCTAA	120
TCTGGGAGCC	TGCAAGTGAC	AACAGCCTTT	GCGGTCCTTA	GACAGCTTGG	CCTGGAGGAG	180
AACACATGAA	AGAAAGAACC	TCAAGAGGCT	TTGTTTTCTG	TGAAACAGTA	TTTCTATACA	240
GTTGCTCCAA	TGACAGAGTT	ACCTGCACCG	TTGTCTTACT	TCCAGAATGC	ACAGATGTCT	300
GAGGACAACC	ACCTGAGCAA	TACTGTACGT	AGCCAGAATG	ACAATAGAGA	ACGGCAGGAG	360
CACAACGACA	GACGGAGCCT	TGGCCACCCT	GAGCCATTAT	CTAATGGACG	ACCCCAGGGT	420
AACTCCCGGC	AGGTGGTGGA	GCAAGATGAG	GAAGAAGATG	AGGAGCTGAC	ATTGAAATAT	480
GGCGCCAAGC	ATGTGATCAT	GCTCTTTGTC	CCTGTGACTC	TCTGCATGGT	GGTGGTCGTG	540
GCTACCATTA	AGTCAGTCAG	CTTTTATACC	CGGAAGGATG	GGCAGCTAAT	CTATACCCCA	600
TTCACAGAAG	ATACCGAGAC	TGTGGGCCAG	AGAGCCCTGC	ACTCAATTCT	GAATGCTGCC	660
ATCATGATCA	GTGTCATTGT	TGTCATGACT	ATCCTCCTGG	TGGTTCTGTA	TAAATACAGG	720
TGCTATAAGG	TCATCCATGC	CTGGCTTATT	ATATCATCTC	TATTGTTGCT	GTTCTTTTTT	780
TCATTCAATT	ACTTGGGGGA	AGTGTTTAAA	ACCTATAACG	TTGCTGTGGA	CTACATTACT	840
GTTGCACTCC	TGATCTGGAA	TTTGGGTGTG	GTGGGAATGA	TTTCCATTCA	CTGGAAAGGT	900
CCACTTCGAC	TCCAGCAGGC	ATATCTCATT	ATGATTAGTG	CCCTCATGGC	CCTGGTGTTT	960
ATCAAGTACC	TCCCTGAATG	GACTGCGTGG	CTCATCTTGG	CTGTGATTTC	AGTATATGAT	1020
TTAGTGGCTG	TTTTGTGTCC	GAAAGGTCCA	CTTCGTATGC	TGGTTGAAAC	AGCTCAGGAG	1080
AGAAATGAAA	CGCTTTTTTC	AGCTCTCATT	TACTCCTCAA	CAATGGTGTG	GTTGGTGAAT	1140
ATGGCAGAAG	GAGACCCGGA	AGCTCAAAGG	AGAGTATCCA	AAAATTCCAA	GTATAATGCA	1200
GAAAGCACAG	AAAGGGAGTC	ACAAGACACT	GTTGCAGAGA	ATGATGATGG	CGGGTTCAGT	1260
GAGGAATGGG	AAGCCCAGAG	GGACAGTCAT	CTAGGGCCTC	ATCGCTCTAC	ACCTGAGTCA	1320
CGAGCTGCTG	TCCAGGAACT	TTCCAGCAGT	ATCCTCGCTG	GTGAAGACCC	AGAGGAAAGG	1380
GGAGTAAAAC	TTGGATTGGG	AGATTTCAAT	TTCTACAGTG	TTCTGGTTGG	TAAAGCCTCA	1440
GCAACAGCCA	GTGGAGACTG	GAACACAACC	ATAGCCTGTT	TCGTAGCCAT	ATTAATTGGT	1500
TTGTGCCTTA	CATTATTACT	CCTTGCCATT	TTCAAGAAAG	CATTGCCAGC	TCTTCCAATC	1560
TCCATCACCT	TTGGGCTTGT	TTTCTACTTT	GCCACAGATT	ATCTTGTACA	GCCTTTTATG	1620
GACCAATTAG	CATTCCATCA	ATTTTATATC	TAGCATATTT	GCGGTTAGAA	TCCCATGGAT	1680
GTTTCTTCTT	TGACTATAAC	CAAATCTGGG	GAGGACAAAG	GTGATTTTCC	TGTGTCCACA	1740
TCTAACAAAG	TCAAGATTCC	CGGCTGGACT	TTTGCAGCTT	CCTTCCAAGT	CTTCTGACC	1800

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
 50 55 60
 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
 65 70 75 80
 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
 85 90 95
 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
 100 105 110
 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
 115 120 125
 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
 130 135 140
 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
 145 150 155 160
 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
 165 170 175
 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190
 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Leu Gly Val Val
 195 200 205
 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
 305 310 315 320
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 450 455 460
 Phe Tyr Ile
 465

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCANACANC GGCAGCTGAG GCGGAAACCT AGGCTGCGAG CCGGCCGCC GGGCGCGGAG	60
AGAGAAGGAA CCAACACAAG ACAGCAGCCC TTCGAGGTCT TTAGGCAGCT TGGAGGAGAA	120
CACATGAGAG AAAGAATCCC AAGAGGTTTT GTTTTCTTTG AGAAGGTATT TCTGTCCAGC	180
TGCTCCAATG ACAGAGATAC CTGCACCTTT GTCCTACTTC CAGAATGCCC AGATGTCTGA	240
GGACAGCCAC TCCAGCAGCG CCATCCGGAG CCAGAATGAC AGCCAAGAAC GGCAGCAGCA	300
GCATGACAGG CAGAGACTTG ACAACCCTGA GCCAATATCT AATGGGCGGC CCCAGAGTAA	360
CTCAAGACAG GTGGTGAAC AAGATGAGGA GGAAGACGAA GAGCTGACAT TGAAATATGG	420
AGCCAAGCAT GTCATCATGC TCTTTGTCCC CGTGACCCTC TGCATGGTCG TCGTCGTGGC	480

CACCATCAAA TCAGTCAGCT TCTATACCCG GAAGGACGGT CAGCTAATCT ACACCCCATT	540
CACAGAAGAC ACTGAGACTG TAGGCCAAAG AGCCCTGCAC TCGATCCTGA ATGCGGCCAT	600
CATGATCAGT GTCATTGTCA TTATGACCAT CCTCCTGGTG GTCCTGTATA AATACAGGTG	660
CTACAAGGTC ATCCACGCCT GGCTTATTAT TTCATCTCTG TTGTTGCTGT TCTTTTTTTC	720
GTTCAATTAC TTAGGGGAAG TATTTAAGAC CTACAATGTC KCCGTGGACT ACGTTACAGT	780
AGCACTCCTA ATCTGGAATT GGGGTGTGGT CGGGATGATT GCCATCCACT GGAAAGGCCC	840
CCTTCGACTG CAGCAGGCGT ATCTCATTAT GATCAGTGCC CTCATGGCCC TGGTATTTAT	900
CAAGTACCTC CCCGAATGGA CCGCATGGCT CATCTTGGCT GTGATTTTCTG TATATGATTT	960
GGTGGCTGTT TTATGTCCCA AAGGCCCACT TCGTATGCTG GTTGAAACAG CTCAGGAAAG	1020
AAATGAGACT CTCTTTCCAG CTCTTATCTA TTCCTCAACA ATGGTGTGGT TGGTGAATAT	1080
GGCTGAAGGA GACCCAGAAG CCCAAAGGAG GGTACCCAAG AACCCCAAGT ATAACACACA	1140
AAGAGCGGAG AGAGAGACAC AGGACAGTGG TTCTGGGAAC GATGATGGTG GCTTCAGTGA	1200
GGAGTGGGAG GCCCAAAGAG ACAGTCACCT GGGGCCTCAT CGCTCCACTC CCGAGTCAAG	1260
AGCTGCTGTC CAGGAACTTT CTGGGAGCAT TCTAACGAGT GAAGACCCGG AGGAAAGAGG	1320
AGTAAAACTT GGACTGGGAG ATTTTCATTTT CTACAGTGTT CTGGTTGGTA AGGCCTCAGC	1380
AACCGCCAGT GGAGACTGGA ACACAACCAT AGCCTGCTTK GTAGCCATAC TGATCGGCCT	1440
GTGCCTTANA TTACTCCTGC TCGCCATTTA CAAGAAAGGG TNGCCAGCCC NCCCCATCTC	1500
CATCACCTTC GGGTTCGTGT TCTNCTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA	1560
CCAAC TTGCA TTCCATCAGT TTTATATCTA GCCTTTCTGC AGTTAGAACA TGGATGTTTC	1620
TTCTTTGATT ATCAAAAACA CAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT	1680
TCCTGTGTCC TCAGCTAACA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCCGA	1740
GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAAGGAAG CGTCTACAGA GGAACGGTTT	1800
CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA	1860
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GGMCCGTGGG CATGGAGATT	1920
TACCCGCAC	1929

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Glu	Ile	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Ser	His	Ser	Ser	Ser	Ala	Ile	Arg	Ser	Gln	Asn	Asp	Ser
			20					25					30		
Gln	Glu	Arg	Gln	Gln	Gln	His	Asp	Arg	Gln	Arg	Leu	Asp	Asn	Pro	Glu
		35					40					45			
Pro	Ile	Ser	Asn	Gly	Arg	Pro	Gln	Ser	Asn	Ser	Arg	Gln	Val	Val	Glu
	50					55					60				
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys
65					70					75					80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
				85					90					95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
			100					105					110		
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg
		115					120					125			
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val
	130					135					140				
Ile	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys
145				150					155						160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe
				165					170					175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Xaa
			180					185					190		
Val	Asp	Tyr	Val	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Trp	Gly	Val	Val
		195					200					205			
Gly	Met	Ile	Ala	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala
	210					215					220				
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr
225					230					235					240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr
				245					250					255	
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val

260	265	270
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr		
275	280	285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu		
290	295	300
Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala		
305	310	315
Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe		
325	330	335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg		
340	345	350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile		
355	360	365
Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly		
370	375	380
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala		
385	390	395
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Xaa Val Ala Ile Leu Ile		
405	410	415
Gly Leu Cys Leu Xaa Leu Leu Leu Leu Ala Ile Tyr Lys Lys Gly Xaa		
420	425	430
Pro Ala Xaa Pro Ile Ser Ile Thr Phe Gly Phe Val Phe Xaa Phe Ala		
435	440	445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln		
450	455	460
Phe Tyr Ile		
465		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3087 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA CGAGGGAAAT GCTGTTTGCT CGAAGACGTC TCAGGGCGCA GGTGCCTTGG	60
GCCGGGATTA GTAGCCGTCT GAACTGGAGT GGAGTAGGAG AAAGAGGAAG CGTCTTGGGC	120

TGGGTCTGCT	TGAGCAACTG	GTGAAACTCC	GCGCCTCACG	CCCCGGGTGT	GTCCTTGTCC	180
AGGGGCGACG	AGCATTCTGG	GCGAAGTCCG	CACSCCTCTT	GTTCGAGGCG	GAAGACGGGG	240
TCTGATSCTT	TCTCCTTGGT	CGGGMCTGTC	TCGAGGCATG	CATGTCCAGT	GACTCTTGTG	300
TTTGCTGCTG	CTTCCCTCTC	AGATTCTTCT	CACCGTTGTG	GTCAGCTCTG	CTTTAGGCAN	360
TATTAATCCA	TAGTGGAGGC	TGGGATGGGT	GAGAGAATTG	AGGTGACTTT	TCCATAATTC	420
AGACCTAATC	TGGGAGCCTG	CAAGTGACAA	CAGCCTTTGC	GGTCCTTAGA	CAGCTTGGCC	480
TGGAGGAGAA	CACATGAAAG	AAAGAACCTC	AAGAGGCTTT	GTTTTCTGTG	AAACAGTATT	540
TCTATACAGT	TGCTCCAATG	ACAGAGTTAC	CTGCACCGTT	GTCCTACTTC	CAGAATGCAC	600
AGATGTCTGA	GGACAACCAC	CTGAGCAATA	CTAATGACAA	TAGAGAACGG	CAGGAGCACA	660
ACGACAGACG	GAGCCTTGGC	CACCCTGAGC	CATTATCTAA	TGGACGACCC	CAGGGTAACT	720
CCCGGCAGGT	GGTGGAGCAA	GATGAGGAAG	AAGATGAGGA	GCTGACATTG	AAATATGGCG	780
CCAAGCATGT	GATCATGCTC	TTTGTCCCTG	TGACTCTCTG	CATGGTGGTG	GTCGTGGCTA	840
CCATTAAGTC	AGTCAGCTTT	TATACCCGGA	AGGATGGGCA	GCTAATCTAT	ACCCCATTCa	900
CAGAAGATAC	CGAGACTGTG	GGCCAGAGAG	CCCTGCACTC	AATTCTGAAT	GCTGCCATCA	960
TGATCAGTGT	CATTGTTGTC	ATGACTATCC	TCCTGGTGGT	TCTGTATAAA	TACAGGTGCT	1020
ATAAGGTCAT	CCATGCCTGG	CTTATTATAT	CATCTCTATT	GTTGCTGTTT	TTTTTTTCAT	1080
TCATTTACTT	GGGGGAAGTG	TTTAAAACCT	ATAACGTTGC	TGTGGACTAC	ATTACTGTTG	1140
CACTCCTGAT	CTGGAATTTG	GGTGTGGTGG	GAATGATTTT	CATTCACTGG	AAAGGTCCAC	1200
TTCGACTCCA	GCAGGCATAT	CTCATTATGA	TTAGTGCCCT	CATGGCCCTG	GTGTTTATCA	1260
AGTACCTCCC	TGAATGGACT	GCGTGGCTCA	TCTTGGCTGT	GATTTAGTA	TATGATTTAG	1320
TGGCTGTTTT	GTGTCCGAAA	GGTCCACTTC	GTATGCTGGT	TGAAACAGCT	CAGGAGAGAA	1380
ATGAAACGCT	TTTTCCAGCT	CTCATTTACT	CCTCAACAAT	GGTGTGGTTG	GTGAATATGG	1440
CAGAAGGAGA	CCCGGAAGCT	CAAAGGAGAG	TATCCAAAAA	TTCCAAGTAT	AATGCAGAAA	1500
GCACAGAAAAG	GGAGTCACAA	GACACTGTTG	CAGAGAATGA	TGATGGCGGG	TTCAGTGAGG	1560
AATGGGAAGC	CCAGAGGGAC	AGTCATCTAG	GGCCTCATCG	CTCTACACCT	GAGTCACGAG	1620
CTGCTGTCCA	GGAACTTTCC	AGCAGTATCC	TCGCTGGTGA	AGACCCAGAG	GAAAGGGGAG	1680
TAAAACTTGG	ATTGGGAGAT	TTCATTTTCT	ACAGTGTTCT	GGTTGGTAAA	GCCTCAGCAA	1740
CAGCCAGTGG	AGACTGGAAC	ACAACCATAG	CCTGTTTCGT	AGCCATATTA	ATTGGTTTGT	1800

GCCTTACATT ATTACTCCTT GCCATTTTCA AGAAAGCATT GCCAGCTCTT CCAATCTCCA	1860
TCACCTTTGG GCTTGTTTTT TACTTTGCCA CAGATTATCT TGTACAGCCT TTTATGGACC	1920
AATTAGCATT CCATCAATTT TATATCTAGC ATATTTGCGG TTAGAATCCC ATGGATGTTT	1980
CTTCTTTGAC TATAACCAAA TCTGGGGAGG ACAAAGGTGA TTTTCCTGTG TCCACATCTA	2040
ACAAAGTCAA GATTCCCGGC TGGACTTTTG CAGCTTCCTT CCAAGTCTTC CTGACCACCT	2100
TGCACTATTG GACTTTGGAA GGAGGTGCCT ATAGAAAACG ATTTTGAACA TACTTCATCG	2160
CAGTGGACTG TGTCCCTCGGT GCAGAACTA CCAGATTTGA GGGACGAGGT CAAGGAGATA	2220
TGATAGGCCG GGAAGTTGCT GTGCCCCATC AGCAGCTTGA CGCGTGGTCA CAGGACGATT	2280
TCCTTGACAC TGCGAACCTCT CAGGACTACC GGTTACCAAG AGGTTAGGTG AAGTGGTTTA	2340
AACCAAACGG AACTCTTCAT CTTAAACTAC ACGTTGAAAA TCAACCCAAT AATTCTGTAT	2400
TAACTGAATT CTGAACTTTT CAGGAGGTAC TGTGAGGAAG AGCAGGCACC AGCAGCAGAA	2460
TGGGGAATGG AGAGGTGGGC AGGGGTTCCTA GCTTCCCTTT GATTTTTTGC TGCAGACTCA	2520
TCCTTTTTAA ATGAGACTTG TTTCCCCTC TCTTTGAGTC AAGTCAAATA TGTAGATGCC	2580
TTTGGCAATT CTTCTTCTCA AGCACTGACA CTCATTACCG TCTGTGATTG CCATTTCTTC	2640
CCAAGGCCAG TCTGAACCTG AGGTTGCTTT ATCCTAAAAG TTTTAACCTC AGGTTCCAAA	2700
TTCAAGTAAAT TTTGGAAACA GTACAGCTAT TTCTCATCAA TTCTCTATCA TGTTGAAGTC	2760
AAATTTGGAT TTTCCACCAA ATTCTGAATT TGTAGACATA CTTGTACGCT CACTTGCCCC	2820
AGATGCCTCC TCTGTCCTCA TTCTTCTCTC CCACACAAGC AGTCTTTTTT TACAGCCAGT	2880
AAGGCAGCTC TGTCGTGGTA GCAGATGGTC CCACTTATTC TAGGGTCTTA CTCTTTGTAT	2940
GATGAAAAGA ATGTGTTATG AATCGGTGCT GTCAGCCCTG CTGTCAGACC TTCTTCACA	3000
GCAAATGAGA TGTATGCCCA AAGCGGTAGA ATTAAAGAAG AGTAAAATGG CTGTTGAAGC	3060
AAAAAAAAAA AAAAAAAAAA AAAAAAA	3087

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACCAAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTANAGGGAA	180
GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240
TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTTGG TGGAAATTAT	300
TGTACATCTT TTAAAATCTG TGTAATTTTT TTTAGGGAA GTGTTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATT TGATTAGTGC	480
CCTCATGNCC CTGKTGTTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC	540
TGTGATTTCA GTATATGGTA AAACCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC	600
ACTGGAGTGT TTTCTTTCCT CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAATT AGCTATAGTA ACTTTTTTCAT TTGAAGATTT	720
CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG	780
ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT	120
AATAGTGCTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300

ACGCCTGGGA TAATTTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCATCATG CTTACAGGGG GAGGCTGTGC GGGAAGAATG CTCCCACACA GNATAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA	120
GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT	180
CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGSCMA CACATCATTT AAGATAGAAA	240
TTTCTGTATC TTTTAATTTY TTTMAAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT	300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA	360
GCTAGGTTTT TTTCATAGST CTTCTTCCAG ATTGAATGAA CGTCTGTTCT AAAATTTAAC	420
CCCCCAGGGA AATATTCAGT TAACTATGTT AAAAACCAG ACTTGTGATT GAGTTTTGCC	480
TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC	516

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATCCCTCC CCTTTTTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120

TAGTGAGCAG	TGAGGATAAC	CAGAGGTCAC	TCTCCTCACC	ATCTTGGTTT	TGGTGGGTTT	180
TGGCCAGCTT	CTTTATTGCA	ACCAGTTTTA	TCAGCAAGAT	CTTTATGAGC	TGTATCTTGT	240
GCTGACTTCC	TATCTCATCC	CGNAACTAAG	AGTACCTAAC	CTCCTGCAAA	TTGMAGNCCA	300
GNAGGTCTTG	GNCTTATTTN	ACCCAGCCCC	TATTCAARAT	AGAGTNGYTC	TTGGNCCAAA	360
CGCCYCTGAC	ACAAGGATTT	TAAAGTCTTA	TTAATTAAGG	TAAGATAGKT	CCTTGSATAT	420
GTGGTCTGAA	ATCACAGAAA	GCTGAATTTG	GAAAAAGGTG	CTTGGASCTG	CAGCCAGTAA	480
ACAAGTTTTC	ATGCAGGTGT	CAGTATTTAA	GGTACATCTC	AAAGGATAAG	TACAATTGTG	540
TATGTTGGGA	TGAACAGAGA	GAATGGAGCA	ANCCAAGACC	CAGGTAAAAG	AGAGGACCTG	600
AATGCCTTCA	GTGAACAATG	ATAGATAATC	TAGACTTTTA	AACTGCATAC	TTCCTGTACA	660
TTGTTTTTTC	TTGCTTCAGG	TTTTTAGAAC	TCATAGTGAC	GGGTCTGTTG	TTAATCCCAG	720
GTCTAACCGT	TACCTTGATT	CTGCTGAGAA	TCTGATTTAC	TGAAAATGTT	TTTCTTGTGC	780
TTATAGAATG	ACAATAGAGA	ACGGCAGGAG	CACAACGACA	GACGGAGCCT	TGGCCACCCT	840
GANCCATTAT	CTAATGGACG	ACCCAGGGTA	ACTCCCGGCA	GGTGGTGGAN	CAAGATGAGG	900
AAGAAGATGA	GGANCTGACA	TTGAAATATG	NCGSCAAGCA	TGTGATCATG	CTCTTTGKCC	960
CTGTGACTCT	CTGCATGGTG	GTGGTCGTGG	NTACCATTAA	GTCAGTCAGC	TTTTATACCC	1020
GGAAGGATGG	GCAGCTGTAC	GTATGAGTTT	KGTTTTATTA	TTCTCAAASC	CAGTGTGGCT	1080
TTTCTTTACA	GCATGTCATC	ATCACCTTGA	AGGCCTCTNC	ATTGAAGGGG	CATGACTTAG	1140
CTGGAGAGCC	CATCCTCTGT	GATGGTCAGG	AGCAGTTGAG	AGANCGAGGG	GTTATTACTT	1200
CATGTTTTAA	GTGGAGAAAA	GGAACACTGC	AGAAGTATGT	TTCCTGTATG	GTATTACTGG	1260
ATAGGGCTGA	AGTTATGCTG	AATTGAACAC	ATAAATTCTT	TTCCACCTCA	GGGNCAATTG	1320
GCGCCCATTG	NTCTTCTGCC	TAGAATATTC	TTTCCTTTNC	TNACTTKGGN	GGATTAAATT	1380
CCTGTCATCC	CCCTCCTCTT	GGTGTTATAT	ATAAAGTNNT	GGTGCCGCAA	AAGAAGTAGC	1440
ACTCGAATAT	AAAATTTTCC	TTTTAATTCT	CAGCAAGGNA	AGTTACTTCT	ATATAGAAGG	1500
GTGCACCCNT	ACAGATGGAA	CAATGGCAAG	CGCACATTTG	GGACAAGGGA	GGGGAAAGGG	1560
TTCTTATCCC	TGACACACGT	GGTCCCNGCT	GNTGTGTNCT	NCCCCACTG	ANTAGGGTTA	1620
GACTGGACAG	GCTTAAACTA	ATTCCAATTG	GNTAATTTAA	AGAGAATNAT	GGGGTGAATG	1680
CTTTGGGAGG	AGTCAAGGAA	GAGNAGGTAG	NAGGTAACCT	GAATGA		1726

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CNCGTATAAA	AGACCAACAT	TGCCANCNAC	AACCACAGGC	AAGATCTTCT	CCTACCTTCC	60
CCCNNGGTGT	AATACCAAGT	ATTCNCCAAT	TTGTGATAAA	CTTTCATTGG	AAAGTGACCA	120
CCCTCCTTGG	TTAATACATT	GTCTGTGCCT	GCTTTCACAC	TACAGTAGCA	CAGTTGAGTG	180
TTTGCCCTGG	AGACCATATG	ACCCATAGAG	CTTAAAATAT	TCAGTCTGGC	TTTTTACAGA	240
GATGTTTCTG	ACTTTGTAA	TAGAAAATCA	ACCCAAGTGG	TTTAAATAAT	GCACATACTT	300
TCTCTCTCAT	AGAGTAGTGC	AGAGGTAGNC	AGTCCAGATT	AGTASGGTGG	CTTCACGTTC	360
ATCCAAGGAC	TCAATCTCCT	TCTTTCTTCT	TTAGCTTCTA	ACCTCTAGCT	TACTTCAGGG	420
TCCAGGCTGG	AGCCCTASCC	TTCATTTCTG	ACAGTAGGAA	GGAGTAGGGG	AGAAAAGAAC	480
ATAGGACATG	TCAGCAGAAT	TCTCTCCTTA	GAAGTTCCAT	ACACAACACA	TCTCCCTAGA	540
AGTCATTGCC	CTTACTTGTT	CTCATAGCCA	TCCTAAATAT	AAGGGAGTCA	GAAGTAAAGT	600
CTKKNTGGCT	GGGAATATTG	GCACCTGGAA	TAAAAATGTT	TTTCTGTGAA	TGAGAAACAA	660
GGGGAAGATG	GATATGTGAC	ATTATCTTAA	GACAACTCCA	GTTGCAATTA	CTCTGCAGAT	720
GAGAGGCACT	AATTATAAGC	CATATTACCT	TTCTTCTGAC	AACCACTTGT	CAGCCNCGT	780
GGTTTCTGTG	GCAGAATCTG	GTTCYATAMC	AAGTTCCTAA	TAANCTGTAS	CCNAAAAAAT	840
TTGATGAGGT	ATTATAATTA	TTTCAATATA	AAGCACCAC	TAGATGGAGC	CAGTGTCTGC	900
TTACATGTT	AAGTCCTTCT	TTCCATATGT	TAGACATTTT	CTTTGAAGCA	ATTTTAGAGT	960
GTAGCTGTTT	TTCTCAGGTT	AAAAATTCTT	AGCTAGGATT	GGTGAGTTGG	GGAAAAGTGA	1020
CTTATAAGAT	NCGAATTGAA	TTAAGAAAAA	GAAAATTCTG	TGTTGGAGGT	GGTAATGTGG	1080
KTGGTGATCT	YCATTAAACAC	TGANCTAGGG	CTTTKGKGTT	TGKTTTATTG	TAGAATCTAT	1140
ACCCCATTC	NAGAAGATAC	CGAGACTGTG	GGCCAGAGAG	CCCTGCACTC	AATTCTGAAT	1200
GCTGCCATCA	TGATCAGNGT	CATTGTWGTG	ATGACTANNC	TCCTGGTGGT	TCWGTATAAA	1260
TACAGGTGCT	ATAAGGTGAG	CATGAGACAC	AGATCTTTGN	TTTCCACCCT	GTTCTTCTTA	1320
TGGTTGGGTA	TTCTTGTCAC	AGTAACTTAA	CTGATCTAGG	AAAGAAAAAA	TGTTTTGTCT	1380

TCTAGAGATA AGTTAATTTT TAGTTTTCTT CCTCCTCACT GTGGAACATT CAAAAAATAC	1440
AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT	1500
TGGGCCCAGG AGTTCACAAG CAGCTTGGGC AACGTAGCAA GACCCTGCCT CTATTAAAGA	1560
AAACAAAAAA CAAATATTGG AAGTATTTTA TATGCATGGA ATCTATATGT CATGAAAAAA	1620
TTAGTGTAAT ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT	1680
TTGGGATTTT AATGCCTTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAAA	1740
AGTTGTAAC T GAAAAATAAA CATTTCCATA TAATAGCACA ATCTAAGTGG GTTTTTGNTT	1800
GTTTGTTTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT	1860
GGCACGATTT TGGCTCACTG CAG	1883

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGGAGTGGA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCNG GGACATAGTG	60
GTACACANCT GTAATGCTCA NCACTKATGG GGAGTACTGA AGGNGGNSGG ATCACTTGNG	120
GGTCNGGAAT NTGAGANCAG CCTGGGCAAN ATGGCGAAAC CCTGTCTCTA CTAAAAATAG	180
CCANAAWNWA GCCTAGCGTG GTGGCGCRCA CGCGTGGTTC CACCTACTCA GGAGGCNTAA	240
GCACGAGNAN TNCTTGAACC CAGGAGGCAG AGGNTGTGGT GARCTGAGAT CGTGCCACTG	300
CACTCCAGTC TGGGCGACMA AGTGAGACCC TGTCTCCNNN AAGAAAAAAA AAATCTGTAC	360
TTTTTAAGGG TTGTGGGACC TGTTAATTAT ATTGAAATGC TTCTYTTCTA GGTCATCCAT	420
GCCTGGCTTA TTATATCATC TCTATTGTTG CTGCTCTTTT TTACATTCAT TTAATTGGGG	480
TAAGTTGTGA AATTTGGGGT CTGTCTTTCA GAATTAATA CCTNNGTGCT GTGTAGCTAT	540
CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTTAATTGT NTCCACATAT	600
AGGTCATACT TGGTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG	660
CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACTTAAGA CTACAGTTAA TTCTAAGCCT	720
TTGGGGAAGG ATTATATAGC CTTCTAGTAG GAAGTCTTGT GCNATCAGAA TGTTTNTAAA	780

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTACTCCTTG CCATTTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA	180
TATTTGCGGT TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCC GGCTGG ACTTTTGGAG	300
GTTCTTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA	360
GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA	420
GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCATCAGC	480
AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGACTACCGT	540
TACCAAGAGG TTAGGTGAAG TGGTTTAAAC CAAACGGAAC TCTTCATCTT AACTACACG	600
TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTTCAG GAGGTACTGT	660
GAGGAAGAGC AGGCACCACC AGCAGAATGG GGAATGGAGA GGTGGGCAGG GGTTCCAGCT	720
TCCCTTTGAT TTTTGG	736

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNNWGTA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACA TTCCNTTAAG GATTACTCAA GCYCCCCTTT TGSTGKNWAA TCAGANNGTC	360
ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTT CTACTTATTG	420
CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA	480
TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT	540
ACTAGGATTT AACTAACAAT GGATGACCTG GTGAAATCCT ATTCAGACC TAATCTGGGA	600
GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT	660
GAAAGAAAGG TTTGTTTCTG CTTAATGTAA TCTATGGAAG TGTTTTTTTAT AACAGTATAA	720
TTGTAGTGCA CAAAGTTCTG TTTTCTTTC CCTTTTCAGA ACCTCAAGAG GCTTTGTTTT	780
CTGTGAAACA GTATTTCTAT ACAGTNTGCT CCAANTGNAC AGAGTTACCT GCACNNCGTT	840
GTCCNTACTT CCAGAATGCA CAGATGTCTG AGGACAACCA CCTGAGCAAT ACT	893

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGAAAATA CTTTNGGGCA CATGAGAATC ACATGAGAAC AAGCTGATGC ATAATTCCTC	60
CTGTGATGGA ATGTAATAGT AATTTAACAG TGTCCTTTCT TTTTAACTGC CTCAAGGATA	120
CAGCAAAATA AAACAAAAGC AATATGAAGG CTGAGAATAG GTATCAGATT ATCATAAAAA	180
GTATAGATCA AAAGGAATCT GGTKCTNAGG TTGGCGCAGC AGCCTCTAGA AGCGACNAGG	240
GAGACTTTTA GAACTACCAT TCTCCTCTAT AAGTGGATCC NANGCCCAGG RAAACTTGAT	300
ATTGAGNACA ATGGCCTTAC TGAAATAACC TGTGATCCAC TCGGNCTCAT CATCTCCACC	360

ACCACCATAA ATTTGATGAG TNCCTATAAT ATTCCANCCA GNGGAAATAC CTGGRAGGTT	420
ACTGAAAGGC NACNATCAGA CNAAAATAAA GNATACCGTA GGTAAATTCT ACAGT	475

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTTCTCNAGA TCTCTTCAAA ATTCATTNTG CGCTATAGGA GCTGGGATTA CCGCGGGTGC	60
TGGAACCAGA CTGNCNCTCC AATGGATCCT CCANACNGGA NGGGGGGTGG ACTCACACCA	120
TTTACAGGGG GCTCGTAAAG AATCCTGTTT TGANTATTNT NCCGTCAATT ACCNCCCCAA	180

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGTAACMA CMAAACCYCA AACTCCTGNA AGAANATGGT TACTTATNGA TNCCATTTNC	60
TTTTTNCACT CTCAGACATA AATATAAACM MANTTTCTAC TGTGGRAAAA CATCTNCAGG	120
GGNCNTTTAN CCATGATCTC TAGNACNANG GGCTNGTGGN TNGTTTTAAT GTCTCTAAGC	180
NACTNGACTA GTTTCTCTTN CACTGAGNAA ACTGCNACAA GTNNTTNCTN CTGNATCTGN	240
ACTGNAATGC TAAGTTNCAA GTNCCAATGA GCTNGTGANT TANYCTTTAT TTNAMCNAAA	300
GTNNTTAATC ANCCNCAGTG TTACTTTGNA AAGCTNCTCC CTGGACAGGC GGCCCNACTT	360
CTAATGTTAT GAATGGGCTG GAGNANCCTC NACNTGAGTT TNNWAAGGNT CAACANCCAA	420
TRGNAANTGT AMCCGACTCT AAATTCCAAC CNATAAT	457

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTGTGCTA GGTAGTGAC TAATCATTCA GTTTATCTCA TTTAATCTNN ATGNAACTCT	60
AAGTCATTCG CTNTGANCNA CACATAACAG ATCTCGCAAC TGNAGTTTAG CGAGGCCAGT	120
TAATTTKCCA AAGNTCATAA TNCTAAGNAG TTCTAGNATG GAGATTCMAA GTCCNACTGT	180
TTAGTCAAGA GACCCTACTG TTAAGTAGTA CCTTTACACT ACTAACTGGG TAANCCATAA	240
NCAATTAATG ATAAAGATTG AGATTACTKC CACATTCTCA CTGGTTATAA ATTAAACNT	300
CAAATAAAAA NTCTTGGCAC TTCTATGGTA ATATTTTTTAT TAGGATAAAC TTTCAAGNAG	360
TGGATNCTAG GTG	373

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 422 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCACACTGN TGGGCCATGG AAGCCATGAG TGTACCACAT GGCCCTGTCC CACTGGCCAC	60
AGTNGATTGG TTGGNTCGGG AGTAGTCACC TGATTCAAGN TGGGCCAATC AGATCCTACC	120
TCCANGGGGT TNNGAATTAG AAAACAGTGA CCCTAGYTAG TNTAGGCNAC TTGAACTGGA	180
GGGCCCATAC ATTCAGGAGC CTTATGGGGC CATGTACACA TGGAAGCAGG AAGANTGAAG	240
GAGGGAGAAG TAGAGGCCAG AAACCCACCT GGGTTCCTGT TTCCCAATGN TAAGTCCCTG	300
CCATGTYCCT GCTCTTCCTG TGGTTNGGAT CTTCAAAGGT TGCTCAAATT NGGGGCAGTG	360
GCCCTGGCAG CTTTTCAAAT CCTYCCATT TTTATTGAAG CTGAAAGACC CTTGACTAGA	420
AC	422

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATTGTTATTT TTCGTCAC TA CCTCCCCGGG TCGGGAGTGG GTAATTTGCG CGCCTGCTGC	60
CTTCCTTGGA TGTGGTAGCC GTTCTCTCAGG CTCCCTCTCC GGAATCGAAC CCTGATTCCC	120
CGTCACCCGT GGTCACCATG GTTAGGCACG GCGACTACCA TCGAAAGTTA ATAGGGCAGA	180
TCTCGAGAAT TCTCGAGATC TCCNTCMAAT TATTACTTCA NTKCGGTAG TGATCAGNAC	240
NAGGCAGTTC TATTGATTTT TCTCCTTTCA TTCTGAGTTT CTCCATAAAT TAATTGGACC	300
TAATCATGTT TKNAATCCTG TCTTTTAGGG GGNANTTGNA CTNTCAAGTG TTTAAAGGGA	360
GGGNCGGAGN ATGATTNTGG ATTGGAGTGA GAGCA	395

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGANTTTCT GGGTNAAAAG GACCTNANAC ATAATATAGT GGA CTTNCAA TAAACACTTA	60
CCAAATGGAN AAATGAACCC CTGGTCACCC CGATCTCACT AGTNCCTNCC CTGAAACCCG	120
ANANATCTGA GTCCTTTTCT CCTTTACTAA CCCTTNCTCC AATCCTGCTC ATGGGAATTA	180
ANGNTGTAAA ATANGCCTGG GGNACCTCGG RCCTCTNCCC TGGGNTCTGT GGGTGGGAGN	240
ACTGTGGAAG CCGTWTCAAT CGCCCCCACC TATGAGAGCC TTTCTNCAGG GCCAGCCATG	300
AACGTCCCCC ATGTNATCAG NATCTNCAGG CTACTGCTGT CCTTCYTGA TWTTTAACCT	360
GGRGGCGGGC CAGGGACAGA AAARGGAGGT GGCAAGATCC TTGAACAAAA GGAGCTATAA	420
AAGGGCGTTG GGGGAAGCAA GGCAAACGGC AGATTAAACA AGCAGGCACC TCAAGGAAAC	480
GTGACGC	487

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 500 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGAGATCT GGCCCATCAT TTAGTTTTAT NGCTTGNAGT NTNTAGNAGA TAAAACATCC	60
ACGTGGATCT NCTCTTAGAG AAATCAANTA CTTTAGGNAT NTGATAGTCA GAGANTGGNT	120
ATCAAATNGA AAGGNATNTN GGTNGANCAG TTAGTTNGYN CCNTTNGNNG AGACCACTGG	180
GNTGTNGASA CCAGATTCMK GGGTNCNAAT CTTANGGTAA TCTNAGAGCC AACACATGGG	240
TCATNTTATS CCCCAAACCTT AGCCACATCT BGTGGGGYTA TGGNGTCACC CCAAGAGCAG	300
GAGGAGCATG GNTGGATGGA AATCCATCTC CACCACTGGA ACCCCAAWTT CTGAATGNAT	360
CACCTGTTAG AGTTTCTTGT YCATAAAATA GCAGGGAATT TAGGAATTTA GTTTTTTTTT	420
AATAGTTTGG GCCTTTTATC CACACTCTCA GGAGCTTAGG ATACTTTTCT CCTTCAGCTC	480
ACTCTGAAAC TCCCTCTGGA	500

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCGAGATCTG TGGTAGTNAC ATGATATTCT GGCAMCTACT TTCATTATCA CCTTTATTAA	60
AATAAATTTA AAGAAAAATG GCAGTATGTT TCTGTGRAGN CCACGAGTAC TCATTTTAAA	120
GGACTCMAGA GTTNCAGRNA AGTAAAAAGR AAAGAGTAAA ATCATTTTCT AANTYTYWYY	180
TTCCAGAAAT AACGATGTTG AGCATTAAGT GGACTTCATT TCATACTCTT TCMMAGNTTA	240
TGTAGGCATA WAWATGTGTG TGTATATACA TATATATGGG TACATCCTTA GAGAAGTTGG	300
CTGGCTAGAT AGACACACNT NAAAAATGGR ATCATACTCT AATKCCATTT NNANTTTANA	360
AAATACATAT TCAGANCCNC TGTNCTTATA NACAGAGTAA NTGAAA	406

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACCCAGTAA AACTTATCTC ATGAGCATAA GGCTGAATGG GATTGACAGC CTACAGAACC	60
CGGATTTTAT CATGAGGGCA TTAGTGGGGG TTGGGGGTTA GGTACTGAAA GTTTAAGGAG	120
GTGAAAGGAA AGCAACTTGT GCCTTACAGG GTCAAGCTAG GTCAAGGAAA TTCCCAGGAG	180
CGTGTGGAAG CTCTCTACCT GATAGGTGAG CTCAAGCTTA TGACCGCCCA AGCTTCTCCC	240
CAAGCTTCCC TTCCACTGCT TCCTCTTGAT TGACTTCCAC AGCAAGGTC	289

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATCAGGAT TTAGTGAGTA AAAATCTCAG GTNTTAACCA TGCCCCTAAA ATGTGCTATN	60
CCAAAGAGGA ACAGGTTACT TGGGAGGAAA AAAGCTGCCT GGGNAACTCC CCNCAATGT	120
TTATTTTAAA TAAAAATGGT NGATGGAAAT ATTTTNTAAA AGAACTTGGG GTNTAATATG	180
GNATACTGCC CATCAAACAA AAAAGGAAAT AAAACTTCNT TCCCATTAT AATAAGTTNC	240
CCACCCTTTA CTATCAAGAT TACAACTTAT TGACCTTTTA TGCTNGCTNG GTTTTTTTGG	300
GACTGCCTAA TCCAATGTTT AAATTTTCTA NGTCTGNATT TCAATGTGGG TAGGAGTNAT	360
TTTTCAA	367

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGTATCTGA	CAGGTAAGAT	TGCTTTTTTAA	AGTTGTTTTTA	AATGCATTAC	ATGACTGAGA	60
AAAGAAAAAT	GCACATTTTA	TTGTTGCAGT	TTAAAATTTTC	ATTTNGNGTG	AAACTAAACG	120
TGAAACAAAA	GGGATAAATG	TGTTTTGNTT	TTGTTTTGGT	TTTACCTGTT	TGGGGTATTT	180
TTTTCTGAGT	TTGTGTAGAA	ACCCGTGTGG	NTACACTGGG	TAATCTTGTC	AGGGNTACMA	240
AMCTTGGGTC	TTGANTTTGG	TTANTTGGNT	TTANTTGGTG	NACCCATGTA	CTTGCTCTTC	300
CNTCCCAGAA	ACATAGCTTG	GTAGGCNAGG	GTTAANCCAG	TGTCGGCGAN	CCCATGTCCC	360
TANCACAGCA	TCTTGTAAGT	TTAATGCACA	ATCGTTCNT	CCCAGGATGG	ANTTATCATT	420
ATAAA						425

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGAGGCGCA	GGAGCCACAA	ATAAAGCAAG	AGCCAGAATC	AGAAGNGGAG	GAAGAAGAAA	60
AGCAAGAAAA	AGRAGRAANA	CGAGAAGAAC	CCATGGRAGA	GGAAGAGGAN	CCAGANCMMA	120
AGCCTTGTCT	GAAACCTACT	CTGAGGCCCA	TCAGCTCTGC	TCCATCTGTT	TCCTCTGCCA	180
GTGGNAATGC	NACACCTAAC	ACTCCTGGGG	ATGAGTCTCC	CTGTGGTATT	ATTATTCCTC	240
ATGRAAACTC	ACCAGATCAA	CAGCAACCTG	AGGAGCATAG	GCCMAAAATA	GGACTAAGTC	300
TTAAACTGGG	TGCTTCCAAT	AGTCCTGGTC	AGCCTAATTC	TGTGAAGAGA	AAGAAACTAC	360
CTGTAGATAG	TGTCTTTAAC	AAATTTGAGG	ATGAAGACAG	TGATGACGTA	CCCCGAAAAA	420
GGAAACTGGT	TCCCTTGGAT	TATGGTGAAG	ATGATAAAAA	TNCAACCAAA	GGCACTGTAA	480
ACACTGAAGA	AAAGCGTAAA	CACATTAAGA	GTCTCATTGA	GAAAATCCCT	ACAGCCAAAC	540
CTGAGCTCTT	CGCTTATCCC	CTGGATTGGT	CTATTGTGGA	TTCTATACTG	ATGGAACGTC	600
GAATTAGACC	ATGGATTAAT	AAGAAAATCA	TAGAATATAT	AGGTGAAGAA	GAAGCTACAT	660
TAGTTGATTT	NGTTTGTTCT	AAGGTTATGG	CTCATAGTNC	ACCCAGAGC	ATTTTAGATG	720
ATGTTGCCAT	GGTACTTGAT	GAAGAAGCAG	AAGTTTTTAT	AGTCAAAATG	TGGAGATTAT	780
TGATATATGA	AACAGAAGCC	AAGAAAATTG	GTCTTGTGAA	GTAAACTTTT	TTATATTTAG	840

AGTTCCATTT CAGATTTCTT CTTTGCCACC CTTTAAAGGA CTTKGAATTT TTCTTTGTCT	900
TKGAAGACAT TGTGAGATCT GTAATTTTTT TTTTTGTAG AAAATGTGAA TTTTTGGTC	960
CTCTAATTTG TTGTTGCCCT GTGTACTCCC TTGGTTGTAA AGTCATCTGA ATCCTTGGTT	1020
CTCTTTATAC TCACCAGGTA CAAATTACTG GTATGTTTTA TAAGCCGCAG CTACTGTACA	1080
CAGCCTATCT GATATAATCT TGTTCCTGCTG ATTTGTTTCT TGTAAATATT AAAACGACTC	1140
CCCAATTATT TTGCAGAATT GCACTTAATA TTGAAATGTA CTGTATAGGA ACCAACATGA	1200
ACAATTTTAA TTGAAAACAC CAGTCATCAA CTATTACCAC CCCCCTCTC TTTTCATCAG	1260
AAATGGCAAG CCCTTGTGAA GGCATGGAGT TTAAAATTGG AATGCAAAAA TTAGCAGACA	1320
ATCCATTTCCT ACTGTATTTT TGTATGAATG TGTTTGTGAA TGTATGTGTA AAAGTCTTTC	1380
TTTTCCCTAA TTTGCTTTGG TGGGGTCCTT AAAACATTTT CCAACTAAAG AATAGAATTG	1440
TAAAGGAAAA GTGGTACTGT TCCAACCTGA AATGTCTGTT ATAATTAGGT TATTAGTTTC	1500
CCAGAGCATG GTGTTCTCGT GTCGTGAGCA ATGTGGGTTG CTAAGTGTAT GGGGTTTTCT	1560
TATTAATAAG ATGGCTGCTT CAGCTTCTCT TTTAAAGGAA TGTGGATCAT AGTGATTTTT	1620
CCTTTTAATT TTATTGCTCA GAAATGAGGC ATATCCCTAA AAATCTCGGA GAGCTGTATT	1680
TAATGCATTT TTGCACTAAT TGGTCCTTAG TTTAATTCTA TTGTATCTGT TTATTTAACA	1740
AAAAATTCAT CATATCAAAA AGTGTAAGTG AAAACCCCTT TAAAAACAAA ACAAAAAAAT	1800
GAAATAAAAT TAGGCAAATT GACAGACAGT GAGAGTTTTA CAAACATGAT AGGTATTCTG	1860
CTCGGCAATT TGTAAGTTTA CATGTTATTT AAGGATAAAG GTAAATCATT CAAGGCAGTT	1920
ACCAACCACT AACTATTTGT TTTCATTTTT GTCTTGTTAGTA AGGTTTATAT CTTGTTTTAC	1980
CTTGGCTCAT TAGTGTTTAA AAATGTACTG ATGATGTGCT TAGAGAAATT CCTGGGGCTT	2040
TCTTCGTTGT AGATCAGAAT TTCACCAGG AGTAAATTA CCTGAAAACG TAAGAAGTTT	2100
TAAACAGCTT TCCACACAAA TTAGATGCAA CTGTTCCCAT GTCTGAGGTA CTTATTTAAA	2160
AGAAAGGTAA AGATTGGCCT GTTAGAAAA GCATAATGTG AGCTTTGGAT TACTGGATTT	2220
TTTTTTTTTT TAAACACACC TGGAGAGGAC ATTTGAAAAC ACTGTTCTTA CCCTCGAACC	2280
CTGATGTGGT TCCATTATGT AAATATTTCA AATATTAAAA ATGTATATAT TTGAAAAAAA	2340
AAAAAAAAAA AAAATTCCTG CGGCCGCAAG GGAATTC	2377

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATTGGAGCTC CACCGCGGTG GCGGCCGCTC TAGNAACTAG TGGATCCCCC GGGCTGCAGG	60
AATTCTCGAG ATCTCCCCCA AGTAAATGAA TGAAAAAAG AACAGCAACA ATAGAGATGA	120
TATAATAAGC CAGGCATGGA TGACCTTATA GCACCCTGTA TTTATACAGA ACCACCAGGA	180
GGATAGTCAT GACAACNATG ACACTGATCA TGATNCCAGC ATTCAGAATT GAGTNCAGGG	240
CTCTCTGGCC CACAGTCTCG GTATCTTCTG TGNATGGGGT ATAGATTARC TGTCCATCCT	300
TCCGGGNATA AAANCTGACT GACTTAATGG TANCCACGAC CACCACCCAT KCAGAGAGTC	360
ACAGGGACMA AAGAGCATGA TCAACATGCT TGGCNCCATA TTTCAATNTC ANCTCCTCAT	420
CTTCTTCCTC ATCTTNCTCC ACCACCTNCC GGGAGTTAAC CCTGGGGTCG TCCATTAGAT	480
AATGGCTCA	489

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGTGCTTC AGTGTTGGCTG ACACAGCAGC ATGGTCTTGA CAAGTTTTCT TCATCCTACC	60
ACAAAATCCC AGTTGGTAAT AGAGACTTTA CTCCTACCTA TCAAAACCAC AAAATGTCCC	120
ATTAGGGGGG GACATGTTGT ACATGTTAGG ATCATTCAAA TAACCAAGAT TATAAGGTGA	180
GGAAAGATGC CCCTAACTGA TTCTTTTGTC TCTCATCTTG TTGGTTCCAG GGACCGAGTG	240
GGGTCAATCT TCTGGTSSTG CCTCTCCAGG TCTCTTCCAG GCCGGTCATA GACGTACTCC	300
CTCTGAGGCC GACCGATGGT TAGAAGAGGT GTCTAAGAGC GTCCGGGCTC AGCAGCCCCA	360
GGCCTCAGCT GCTCCTCTGC AGCCAGTTCT CCAGCCTCCT CCACCCACTG CCATCTCCCA	420
GCCAGCATCA CCTTTCCAAG GGAATGCATT CCTCACCTCT CAGCCTGTGC CAGTGGGTGT	480
GGTCCCAGCC CTGCAACCAG CCTTTGTCCC TGCCCAGTCC TATCCTGTGG CCAATGGAAT	540
GCCCTATCCA GCCCCTAATG TGCCTGTGGT GGGCATCACT CCCTCCCAGA TGGTGGCCAA	600

CGTWTTTGGC	ACTGCAGGCC	ACCCTCAGGC	TGCCCATCCC	CATCAGTCAC	CCAGCCTGGT	660
CAGGCAGCAG	ACATTCCCTC	ACTACGAGGC	AAGCAGTGCT	ACCACCAGTC	CCTTCTTTAA	720
GCCTCCTGCT	CAGCACCTCA	ACGGTTCTGC	AGCTTTCAAT	GGTGTAGATG	ATGGCAGGTT	780
GGCCTCAGCA	GACAGGCATA	CAGAGGTTCC	TACAGGCACC	TGCCCAGTGG	ATCCTTTTGA	840
AGCCCAGTGG	GCTGCATTAG	AAAATAAGTC	CAAGCAGCGT	ACTAATCCCT	CCCCTACCAA	900
CCCTTTCTCC	AGTGACTTAC	AGAAGACGTT	TGAAATTGAA	CTTTAAGCAA	TCATTATGGC	960
TATGTATCTT	GTCCATACCA	GACAGGGAGC	AGGGGGTAGC	GGTCAAAGGA	GCMAAACAGA	1020
YTTTGTCTCC	TGATTAGTAC	TCTTTTCACT	AATCCCAAAG	GTCCCAAGGA	ACAAGTCCAG	1080
GCCCAGAGTA	CTGTGAGGGG	TGATTTTGAA	AGACATGGGA	AAAAGCATTG	CTAGAGAAAA	1140
GCTGCCTTGC	AATTAGGCTA	AAGAAGTCAA	GGAAATGTTG	CTTTCTGTAC	TCCCTCTTCC	1200
CTTACCCCTT	TACAAATCTC	TGGCAACAGA	GAGGCAAAGT	ATCTGAACAA	GAATCTATAT	1260
TCCAAGCACA	TTTACTGAAA	TGTAAAACAC	AACAGGAAGC	AAAGCAATGT	CCCTTTGTTT	1320
TTCAGGCCAT	TCACCTGCCT	CCTGTCAGTA	GTGGCCTGTA	TTAGAGATCA	AGAAGAGTGG	1380
TTTGTGCTCA	GGCTGGGAAC	AGAGAGGCAC	GCTATGCTGC	CAGAATTCCC	AGGAGGGCAT	1440
ATCAGCAACT	GCCCAGCAGA	GCTATATTTT	GGGGGAGAAG	TTGAGCTTCC	ATTTTGAAGTA	1500
ACAGAATAAA	TATTATATAT	ATCAAAAGCC	AAAATCTTTA	TTTTTATGCA	TTTAGAATAT	1560
TTTAAATAGT	TCTCAGATAT	TAAGAAGTTG	TATGAGTTGT	AAGTAATCTT	GCCAAAGGTA	1620
AAGGGGCTAG	TTGTAAGAAA	TTGTACATRA	GATTGATTTA	TCATTGATGC	CTACTGAAAT	1680
AAAAAGAGGA	AAGGCTGGAA	GCATGCAGAC	AGGATCCCTA	GCTTGTTTTT	TGTCAGTCAT	1740
TCATTGTAAG	TAGCACATTG	CAACAACAAT	CATGCTTATG	ACCAATACAG	TCACTAGGTT	1800
GTAGTTTTTT	TTAAATAAAG	GAAAAGCAGT	ATTGTCCTGG	TTTTAAACCT	ATGATGGAAT	1860
TCTAATGTCA	TTATTTTAAT	GGAATCAATC	GAAATATGCT	CTATAGAGAA	TATATCTTTT	1920
ATATATTGCT	GCAGTTTCCT	TATGTTAATC	CTTTAACACT	AAGGTAACAT	GACATAATCA	1980
TACCATAGAA	GGGAACACAG	GTTACCATAT	TGGTTTGTA	TATGGGTCTT	GGTGGGTTTT	2040
GTTTTATCCT	TTAAATTTTG	TTCCCATGAG	TTTTGTGGGG	ATGGGGATTC	TGGTTTTATT	2100
AGCTTTGTGT	GTGTCCTCTT	CCCCCAAACC	CCCTTTTGGT	GAGAACATCC	CCTTGACAGT	2160
TGCAGCCTCT	TGACCTCGGA	TAACAATAAG	AGAGCTCATC	TCATTTTTAC	TTTTGAACGT	2220
TGGCGCTTAC	AATCAAATGT	AAGTTATATA	TATTTGTACT	GATGAAAATT	TATAATCTGC	2280

TTTAACAAAA ATAAATGTTC ATGGTAG

2307

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCAGCTATT TACATGGCCT CACAGGCATC AGCTGAAAAG AGGACCCMAA AAGAAATTGG	60
AGATATTGCT GGTGTTGCTG ATGTTACAAT CAGRCAGTTC TATAGACTGA TCTATCCTCG	120
AGCCCCAGAT CTGTTCTTCA CAGACTTCMA ATTKGACACC CCAGTGGACA AACTACCACA	180
GCTATAAATT GAGGCAGYTA ACGTCMAATT CTTGANNACM AAACCTKNCC TGTTGTACAT	240
AGCCTATACM AAATGCTGGG TTGAGCCTTT CATAAGGNAA AACMNAAGAC ATGGNTACGC	300
ATTCCAGGGC TKGANTACTT ATTGCTTGGC ATTCCTGTAT GTA	343

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAGGGCTAA CCAGCCACTG CACCAAAATT AGTCCTTACA TTATAATACT CTGGCCATTG	60
GAAGAGAAAA ATGGGAAAAT TCAACAATTT GAAAGACTAT GATCCCTCTG GCTCATGATC	120
TACTGACCAG AATGAAGTCC TGAAGGATTT CCTTCTGTTA TGTTATCTAC CCAGCTAATC	180
TCAAACAAGA GGAGCTGGAA AGAACAAAGC CCCATGAAGC TACCCCTAGA CCCAGAAAGC	240
CAAGAACAGG GCCAAGAAAA TGAACAGCAG ACAAGCCTGA AATAGAAGTG GNACAGACAT	300
GTGGNAAGAC CAAGTACACC CAGTTNGGTG GTAAAGATTG CGATATCAAG CTTATCGATA	360
CCG	363

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTACATGGT TTCTTGNCCA CCCASCAC CTTTCCCAT CTCTACCGGY TGATAGTCTC	60
TCAGNTAGTA GACCTTTTCT NGTTTAGRCA GGGCCACNTT TTAAAAACT CCAGACGGGT	120
ACCCTCCATG TKGMAGGCGA CGTGGCCCTG GATCACTCAA CTGANTGTCA TNKGANTGGT	180
GCCCCAGAG TGAGGACAAT GGTGNAGCCC TCCTAAGGCC CTNCCTGAGT GTCCCTCCTT	240
CATGAAGATG ATTCTGAGGN TTCCCAGGCC TNCACCCTTC TTKGAAARCC CATAGNAGTT	300
CATATGNACT NCTCTNCTAT GCTCACCAA CTCTNCCTTC ATCATACTTG GGGGATGTGT	360
GT	362

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCATGTAA TTACAGTTAC GATATATGAA ACGTACAAAA TATTATGAGT ATATAATATG	60
GGGAGACTTA ATCTAGTTTG GGGGATCAGG GCACATTTCT CTAAGAAAGT GACATTTGAA	120
TTGAGCTCTG AAGGATAAAT AGACATTACC CAGAAGAATA AAATGATGGG GAAGAAGGAG	180
GACATTTTCC GTAGATTTCC AGTGGCCCN CTTGATCCCT TATCCACTCA TCAC'TNAGGA	240
GGATATTAAA TKCTATAGAA ATGGRAGRAA GACMMAAAGA GACCCTNATA TCTCGAGAGG	300
ATCCAGCMAA ATTCCAAGAG ACACAACAWT AAGAACTNG GAAGGAAGAG AAAAGGCMMN	360
NNAGGNAAAA GAAAGACAAG GAAATTNWN NAGNACGGAG AGAAAGAGAG AGGGAGCGTN	420
NAAGGGNACG AGAAAGGCGA GNACGGGGAC GAGAAAGGN AAGAGNACGT AAACG	475

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGAAATAAAT GAGATCTCAG TGGTGGTATG GATTGGACTG ATCTCTGTAA CTGTGTNTGG	60
AAAAAGGACC GGAAAATGAA AGCCAGATCC CAGTAAGGGG TAGAGAGGGG CCAAGAGAAC	120
TGAACATCTG GGCTGCCGGA GAAATCAAAG TCTAGGAAGT AAGAGGTAAG AGTGTACTAC	180
AGGGGACATA CCCCAATCTC TTGGTTCCT CCCTCTNCCT TCCTCTCCCA GAGACCCAGG	240
TCCCTGGGAC TATNTTGGAT CTGTCTCTGA AGCTGAAAAA CAAAAGGCAG AGGAGACAGT	300
CGGNTCTAAG TGACCAATCT CAAGCCAGCT TGGTCAGAA TCCTAA	346

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAATCCAGTG CAGGCAACAT TATGTGGAAA TAGAAACAGG GCTCCTGCTA GGAGATTGAN	60
ATTCTGGCTT TCCTTTGGAA CCCCTCACTG ACTCATCGCC CCTGAANCAG GANCCANCAG	120
GTNCCAAGGC TCCCCTGCTC CTNTCCCTNC CCCAGGGCGA GATAGGAARC CGGAARCCTG	180
GGCAGGCTGA RCCCANCCGA CTGGAACCAG GGNAGANCCT GTGGGTGGGT GGNAGGGAGG	240
GAAGGAGGCC AGATTCTCTC AGAACTGGGG RAGAGAACAG GTTTTGAAG TTGGGGGAGG	300
GTTTGGGTTT CACAGTGATG GTTTCATGAN ACCCTGGAGG GTTNCACACT CCTGGTKCAN	360
TTTTGNTANT CGTNCTTTGA ANACARNCCG CTTCCTTTCA ACCCTCCNCN TAAAAAGTTT	420
TGATNTTTTA AGG	433

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCAAGAGCC CCCAGTTTAT GNTAACTCTC ATGACAAACA CAATTTTAGT ACCTCTCACT	60
ACCAACTATC CAGGAACCAG GANTCACCTA TTACTACGGT TCCAGCAGAA TGGGAATCCC	120
ATTCTCGGAT ATCCAGGGTA AATCCCTGAC CATGTGAGAG GAATCCTAGT GCCCCAACAA	180
CCTCACCCCC TGACTCCTCC TCAANGGCTC TGCCAAGTCA ACAAAAAAAT CCTCTACATT	240
TACACTATCT GTAAAGCCAA AGACCAGCGT CAACCTAAAT GTCCATCAAT AAGGGAATGG	300
TTGGATAAGT AAAAATTATG CAGCTGTAGG AAGGAATGAA GAATGTCTAT	350

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAGGGAACA AAAGCTGGTA CCGGGCCCCC CCTCGAGGTC GACGGTATCG ATAAGCTGGA	60
TATCGAATCC TCGAGATCTA CCTAAAAAAA AAAAATTAAC TTCCCAAATG TGGGAGTCTA	120
CTCTGTTCCC TCCTNGTNTT TATTNCTGTN TACTTTYCTA ANATGGTTAA AATGTGTAAN	180
CAATATGTGT CCTTTNACTN KGGKGTGAAC ATTTTTYCTA TTATAAATYC TWAGAAAATA	240
TTNCTATGGN TATGAGATAT TKGATTCCAA GTGCCTKGTA ATTTACTYCT CAAATGTCCC	300
TGATGTKGGA NATTKGTTNC TAGTGTTYCA CTATTTAAAA AAACAGNAAT ATCTGTCTNT	360
ATGCTNAGAG CTTNTYCAGT TTYCAAATTA TTNCCTTAGG GTAAAATCCT AGAAGTAGAA	420
TTTTTGGGGC AAATTATCTA CATATTTATA ATTGTCTTGG TATTCCAAAT CTCGTTTTTC	480
AAAAGCTTAT ATCAATTTGT ACTTAACACC AG	512

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATTTAAGATG ACTGGGGGTC TCTNCCTAAT CCCATACTCC ACTGGAGAGG ANAAGTGGGA	60
AAGGTTGGTC TAGTTARGGT NGNTGGGGAC CCTCCCAAGA GCTGNAGAAG CAGAGATAAG	120
NAGAGCCTNC TNCTAAATCC ACATGGNCCT YCCAAGGNTC TCATCCTCTA GGACCTACCA	180
CTNCTCAGTC TACTTACTTG TCTYCTGANA TGCTTTCTNG AGGGGNAGAA AACAAAGGAA	240
GAGTAATAAC AAGCAGNAGA AACTGCAGAG AATGNAAAAT AAGTCCATAG GAGAATGTTG	300
NAAATAGAAT CATCCNCCTT TACATATTGT CACTCCAGGA AACTGCCAA GAACCACTCA	360
TTCCTCTAGA TACAMTTCCT GTAGGATCCY CCCAGACTTC CTCCCTTAAG CACGTCAGTA	420
TTCTCCTTAT TCTCCCTTCA TTTCAACCCT	450

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGATCTGC CCCAGCCCAC ATTTCTTTTG TTGAATGAGT AGAGAAGACT GAGAAGTATC	60
ACTCACCCGT GATGTGGTTT GTCCCTTTTC CAGCCAGTGT GTTGGTAATA AAAGTCACCT	120
TTCAGAGCTT TGGTCCCCGT AATGCCCGTC TTTCTGTGT CCAGGAATAA CCTTTGNTAC	180
TAGGCAGTCC TCTGAAAGAT TTGTAGAAGG TTAAAGTGGA AAGGGACTTG GAAGCTCATA	240
GAATCCATGC CTCTTCTTTT AGCATCAAGG AATTAGAAGT CCTGAGAGAT GAAGAATGTT	300
GTCTTCCCAA CTCAAACCCA TTTCTTGAAG CCATTTCCCT GGTTACTGNA TTGGCCACAA	360
CCCTTCCCCC TTGNTATCCT CATCCTGCTA ATGCTGTTTT TAATGGCCTG CCAGTCTGGA	420
TTTGTCTTTG GCAACCAAC AATTTTGCTT CACAAGATTC CTACTTAAGG GAAGAGAGGG	480
GCTCCTCATT TNTCACTTGT ACAAGAGCAG GGCTGGTCAG CTTTACACAG GTGTCAGATG	540
AACCGTCACA ANCCAGANTT NCATGTTGGC CTCAGGAGGG CTTNAGGTC CAACATCTCG	600
ACGTAAGGAG CGTTCCAGT TCTTTCATGC TCAGATAACA GTNCTAACTN CAGCTGTTTC	660

ATCCCNAATC CCTANTTGAG GTCTTAACAT CTATTCCATT TTKCCNACMA GGGTTATNCT	720
GTTAACCCCTC TNCACCAGAN TTAGANCTGA CTGATNCACT TCCTAG	766

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATACTTGT ATAGTTCKNT AAGATAATCA CTCTCTCACT CAGACATNNG GNGRARNGCC	60
CNTCGATCAC TTGGGANAGG NGA CTTGCM TGT TTAATGA TTGTCANCCM NANAANTAAG	120
CTNACAGGGC AAAACAGCC TYANGTCAGT TCTNTCTCCC TAATCCTCTA GRAKNAAATC	180
NNAWRNTRNN ACTCTGNNTC TGTGCCATNA NANATNTTNC ANTTGTATTT ATGNACTCCA	240
CATNGAGTAC ACCTCACTAA WTNTNCTNCT GGGNAACNCC CSCMCCANTT TTTNNTTGNT	300
GANANACARC AATGCTGGCA TACNGTG	327

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCAGACTTTC ATA ACTNGTG TTATTATGAA GATTAGAGTN CTGAAGCTTA CTGGATTAGA	60
AGAGNACGAG GGGGTAGCTG CCCCAATATA TTCTAATTTT TCTKGAGGAC CACCAAATNG	120
GMAGAGTGTC TCTGATAGGG AAAAGGAAGA GTTGGAAGGN ATCTTAGCCT CTAGGANAAA	180
AGAACCATTT TTATTGGCCA CCAAAGTTAC ATCTAGTKGC CTACAAATTT ATNTCCAAAC	240
TCCTTATCCT GCCAATTCAG GGTCTGNAA ACTGATGCCA AACTATAGTT TAGTCTNCTA	300
TCACATGACT GCATTATACA TACCCAATTA TCTGGGMAAA CAGACCTGAT CCAAACACAG	360
TTKGGTNCTT TCCTTNCCTT NCCTTKGTTT AGCCTGTYCC GTCTACTNGG GGTGTCTTKG	420

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTTTTTCCA CCAGACTTAC CAAATTTTAG ATGNATGGAA GAACTGTAAA TNCCCATAAA	60
GNTAATCTAT NCATNGACCC CCACCATTAT GATAGAGATC ATNTGGTGAN TAATGAAAGA	120
TGAAACTCTC AGCTGGGAAA GTAANAAGGA ATAGGATGTA AGTATGAGCT CCTGTTTTTTT	180
ATTATNTTTA TGGATGCCCC CTCAGAAAAA TATGNAANGG GGTAAGTAC TNGGAAATGG	240
GTNTTTTATG NATAGTAAGT CCCACTCACG AGGTTT	276

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGAGATCTA AAGCAGATGN AGACTTTNCA CNAATAAAT TTACTGCTTT TTTYCTGTGA	60
NATAAGTTNC GAGAAGGAAA GCTTTKGATT NCTRATGAG TYCAGTGGAT TATYCTNAGN	120
ACTAGAGTKG NKGTKGAAGN CATGGNACAT TTATATAGWT YWTTCAAGTTC TACACTAAAT	180
GATGGAAGAA TGAGAAATCC TATATGACAA ATAGAAAAGT YCATYCTYCA TAATTGAGAA	240
CATTGAGCAG TTGGATTACC AAGATCTCGA	270

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTAGTTTTA	GACTAGTTTC	ATTATACTAC	CAGTTTCTAA	TATGTTGGTT	TTTTATTAC	60
TATTTGATAT	ATTTGTTTTA	ATATATGTTT	TTGTTTTAGC	AGGTAAAAGA	ATCATAACAA	120
ATGTTTTTAA	AAGAACATTA	TTATTCTTTA	ATAACTGTCT	TTTTATGCAT	TTGGCATGCC	180
AACTTTTTTC	ATTAACATCT	TGGGTATTTT	ATAAAAAGAG	GGAAAGCTCA	ATGTTTAACA	240
GGTAGCTTTT	CTTAGGAGCT	AAATTAAATA	TTTAACAAAT	CTCCTTCCCT	TCNCCCTTCC	300
CCATCCCTCA	AAGNATGGGT	GNANTTATCT	TTAACTTTTG	GGCTNGCATC	CNTGNAAGCT	360
TATGGNTANT	CATAGTCTNA	CMAAACTAGG	GTCACCNAAC	TTGGCAGCAG	AAATAATCTA	420
GTCTTACTGT	GATAACTACC	CAATTACTTT	ATTATTTTTT	CAGTTNCAGT	TCCAAATGTT	480
TTGTGGNAAN	AATTTTNNCT	GTTTGTGATT	TTCCAAGCTT	AGAGGGGGAA	ACCAACTTTC	540
CAGTGTGGA	GAGCACTGNA	TAGTTTATGN	ATTGTGTAAA			580

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTTTCTTAA	NACAGAAAAA	AATTTACTGA	TNGGACATTG	TTCTAAGTGT	ATTATTGTAT	60
TAAATGGATC	ATTTAATTTA	ATCTTCATAA	CTGACATAGG	AGTTGAGTAA	CTTGTGTGGT	120
CAAATAGCTA	GTAAGTGATG	AGTAGGCTGG	GCGCAGTGGC	TCAAGCCTGT	AATCCCAGCA	180
CTCTGGGAGG	CTGAGGCAGG	CAGATCACTT	GAGGTCAGGA	GTTTGAGACC	AGCCTGGNCA	240
ACATGGNAAA	ACCTCGTCTC	TACTAAAAAT	ACAAAAATTA	GCTGGGCGTG	GTGGGNGCGC	300
ACTTGTAGNC	CCAGNTACTC	GGAAGGCTGA	GGCAGGAGGA	ATCGCTT		347

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
GCTCATCATG CTTACAGGGG GAGGCTGTGC GGAAGAATG CTCCACACA GNATAAGAA      60
TGCTCCCGCA CAGGATAGAG AATGCCCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA    120
GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGN ATAGAGAATG CTCTTCACCT    180
CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGGCAA CACATCATTT AAGATAGAAA    240
TTTCTGTATC TTTAATTTT TTTCAAAGTA GTTTTACTTA TTTNCAGATT CTATTTCTTT    300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACAAACAAAA    360
GCTAGGTTTT NTNCATAGGT CTNCTCCNN ATTGAATGAA CGTCTNTCCT CAAATTTANC    420
CCCCCAGGGA                                     430
```

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
CAAACCTAT GNGAAATGGA AAGGAACTA TTCTAAAGCA TAAAAGGTAG AAATATATAT      60
ACCACCCATC AAGAAAGATT ATTTTGTGTG AACTCAAGTC ACCAGAGTGG CTAAAGCCCA    120
GTAGAATGGA AATGATTATA TGGAAGGTGA GGCCAACGGG ACCAGAACAT ACTGTGATAG    180
ACAGNAAGGA GCTGTCTATC TTCTATTCTC CCACAGAAGG AGGTGACTAA GTCANCTGCC    240
CAAGCAATGT TATATCTGCA ATTGATGTNC AGCAGTACAA GTCTGAACAA CTTGGATTGG    300
NTGATTAATG TCCACANTAA ACATACAAGT CNTAATAGCT ATCTCTATAT AGTCTTTGGG    360
TNTTTACAAG GCACTGNCAC ATNATCTCAC CTATTCCTCC                               400
```

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGNATCCAGA ATTGAGTGNA GNGTTCTCTG GNCCACAGTC TCGGTATCTN CTGTGAAATG	60
GGGTATAGAT TCTACAATAA AACAAACACA NNGGCCCTAG GTCAGTGTTA ATGGAGATCA	120
CCANCCACAT TACCACCTCC AACACAGAAT TTTCTTTTTT TTAATNCAAT NCGTNTCTTA	180
TAAGTCACTT TNCCCCAACT CACCAATCTA GNTAAGAATT TTTACCCTGA GAAAAACAGC	240
TACACTCTAA AATTGCTNCA AAGAAAATGT CTAACATNTG GAAAGAAGGA CTTAACATGT	300
GANGNAGACA CTGGCTCCAT CTAGNGGGTG CTTTNTTTTG AAATAATTAT AATNCCNCAT	360
CAAATTTTNG GGGGNTACAG CTTATTAGGA ACTTGTTATA GAACCAGATT CTGCCACAGA	420
ANCCACGTGG GTTGACAAGT GGTGNCAGA AGAAAGGTAA TATGGCTTAT NATTAGGGNC	480
TCNCATCTGC AGAGTAATTG	500

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAATGCTTG ANNCAAATGT CATCTAGTTC CATCTCTACG ACTCTCATGG GGTCCAAAGA	60
AGAGTTTTAN TTGAGTTTTA GAATGTGAAG TTGTGAAGTG TCTGAAAAAC TACATGGTGN	120
TCTGAAAGNC AAACTTTTAG CCTTGGGGGA GAGCATCTAA GACAGNAGGT GAAGGGNAGG	180
GGTTAGAACT AGAGGGATTG AAGAATATTA TCCATATAGG TTAGGGTTAG GTNNGGCAAC	240
GTTTTATAGA ACAAACATTG GCAAGCTACA GCCACAGGCC AGATCTGTCT NCTACCTTCC	300
CACAAAGGTG TAATAACAAA GTTATTACACA AATGTGTGAA TAAACTNNCA TTGGAAAGTG	360
CCCACGCTCC TNGGTTTATA CATTGTCTGT GGCTGCTTTC AACTACAGT AGCACAGGTG	420
AGTGTNTGCA CTGGAGACCA TATGCCCCAT AGAGCTTTAA	460

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
ATCAAGCAAC AGTGTGTTAT GCCTATACTC CATGTTTATA TGTGTGTATT AAAAAATGTA      60
TTTGTATATA TGTGTATGTA TAAGTGTGTG TGTGTGTATG ATGATTCTNC TCCCGNTTTG      120
AAGGTGAAAG AAAGCACACC TTTATTTAAG CATAAACTTT GGGTTTCAGA TACTGTCTGG      180
AAAAATGATT TATCTCCAC TTTGAAATTC CAAAATACGT ACATATATTT TTTTTTCTT      240
TTCTTTTTTA GTTTNAGGGT CTTGCTGTGT TGCCCAGGCT GGAGTGCAGT AGTGTGATCA      300
TAGNTCACAC AGNCTCTAAC TCCCAGGNTC AAGNTATCTT CCTGCCCCAG NCTCCTGAGT      360
AGNTGGGACT                                     370
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
CAAAAAATCA AAGGGAAGNT GGAACCCCTG CCCACCTCTC CATTCCCAT TCTGCTGGTG      60
GTGNCTGCTC TTCCTCACAG TACCTCCTGA AAAGTTCAGA ATTCAGTTAA TACAGAATTA      120
TTGGGTTGAT TTTCAACGTG TAGTTTAAGA TGAAGAGTTC CGNTTGGTTT AAACCACTTC      180
ACCTAACCTC TTGGTAACGG TAGTCCTGAG AGTTCGCAGT GTCANTGAAA ATCGTCCTGT      240
GACCACGCGT CAAGCTGCTG ATGGGGGACA GAACTTCCG GGNCTATCAT ATCTCCTTGA      300
NCTCGGCCCT CAAATCTGGT AGTTTCTGCA CCGAGGGACA CAGTCCACTG CGATGAAGTA      360
TGTTCAAAAT CGNTTCTTT AGGGAACTCC TTCCAAAGTC CAATAGTGNA AGGTGGTCAA      420
GGAAGGATTT GGAAGGAAGN TGNAAAAGTC AGNCGGGAAT CTTGATTGG NTAGNTGTGG      480
ANANAGGAAA TCACTTGGCC                                     500
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAGAGGT CTCCTAACAC CCAGACAGTG TAAAAATCCA GTTTTCTTC CTTTGGNNG	60
GAGACAGAGT CTCGCACTGT AGCTCAGGCT GGAGTGCAGT GGCAC	105

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGTCCCAGCT ACTCAGGAGG CTGGGGCAGG AAGATAGCTT GAGCCTGGGA GTTAGAGGCT	60
GTGTGAGCTA TGATCACACT ACTGCACTCC AGCCTGGGCA ACACAGCAAG ACCCTAAAAC	120
TAAAAAAGAA AAGAAAAAAA AAATATATGT ACGTATTTTG GAATTTCAAA GTGGGAGATA	180
AATCATTTTT CCAGACAGTA TCTGAAACCC AAAGTTTATG CTTAAATAAA GGTGTGCTTT	240
CTTTCACCTT CAAAGCGGGA GAAGAATCAT CATAACACA CACACACTTA TACATACACA	300
TATATACAAA ATACATTTTT TAATACACAC ATATAACAT GGAGTATAGG CATAACACAC	360
TGTTGCTTGA TAAAATATAG GGATCC	386

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATATTTNAT CAAGCAACAG TGTGTTATGC CTATACTCCA TGTTTATATG TGTGTATTAA	60
AAAATGTATT TGTATATATG TGTATGTATA AGTGTGTGTG TGTGTATGAT GATTCTCCTC	120
CCGNTTGAAG GTGAAAGAAA GCACACCTTT ATTTAAGCAT AAACCTTGGG TTTCAGATAC	180

TGTCTGGAAA AATGATTTAT CTCCCACTTT GAAATTCCAA AATACGTACA TATATTTTTT	240
TTTTCTTTTC TTTTTTAGTT TNAGGGTCTT GCTGTGTTGC CCAGGCTGGA GTGCAGTAGT	300
GTGATCATAG NTCACACAGG CTCTAACTCC CAGGNTCAAG CTATCTTCCT GCCCCAGNCT	360
CCTGAGTAGG TGGGACT	377

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGCAGTAAG CCACGTTTCAT GCCACTGTAC TCTAGCGTGG ATGACAGAGA GAGATCCTGT	60
CTTTGGAAGA AAAAAACAAA AAGAAAAAAA AAAGAGTATG GCCATGGCCT TATAATATAG	120
AAGGGGTCAC ATATTAATCT CTGAAAATGG ATCTCTTGTTG GGCTTTCATA CAAGGCAACA	180
GCCACAGAGT ACGTACCTGA AAGCTGCCTG GGNTTAATGG CTGGNAGTAT GTTCTAACTN	240
GTTTCAGGNAC CCATGTCACN ACTGGTGGTT ACAGAATGTG AATCTCACAC TGTCCNAAAT	300
CGGTTTTTATT TTTAAAANGA ATAATTCTAN TACATTACCT TATAAAAAGT AGGTAACCTA	360
ATTTTGGNNTT TTAAAAGTGA ATTGAGGGCA GATGCAAGTG GNTCACACCT ATTAATCCCA	420
AATACCTTGG AGAGGGCAAG GTAGGAGGAT TGGTTGGAGC CCAGGAGTCC AAAGACCAGG	480
CTAGGGAATA TTGNAAGAAAN GTCCTCTCTA CAANAAANAA T	521

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTGCANGAAG CTTTTNTTNC TTTTNGGNGG AGACAGAGTC TTGCTGTGTC ANCCCAGGCT	60
GGGGTGCACT GGNACAGTCA TAGCTCACTG CAACCTTGAA CTCCCTGGNT CATGCGATCC	120
TCCCACTTCA GCCTCTCAAG TAGCTAGAAC TACAGGTGTG CACCACCATG CCTGACTAAC	180

TTGTTTATTN GNGGGAGAGA GAACGNTCTT GCTATATTGC CTAGGCTGGT CNTTGAAGTC	240
TTGGGNTNCA AGCAATCCTC CTACCTTGGC CTCTNCAAGG TANTTGGGAT TNATAGGTGT	300
GAGCCACNTG CATCTGGCCT CAATTCACCTT TAAAAATNCA AAATTAGGTT ACCTACTTTT	360
TATAAGGTAA TGTATTAGAA TTATTCTTNN NAAAAATAAA ACCGATTTGG GAAAGNGTGA	420
GANTCACATT CTGTAACCAC CAGTGGTGAA ATGGGTCCCC GAACAAGGTA GAACATACTC	480
CCAGCCATTA ACCCCAGGGA GNGTTCAAGT CCGTNC	516

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGATCCTGTT TCTTAAACA GAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
TTGTATTAAA TGGATCATTT AATTTAATCT TCATAACTGA CATAGGAGTT GAGTAACTTG	120
TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGGCGC AGTGGNTCAA GCCTGTAATC	180
CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACCTGAGG TCAGGAGTTT GAGACCAGCC	240
TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GCGTGGTGG	300
GTGCGCACTT GTAGTCCCAG CTACTCGGAA GGGTTGAGGC AGGAGGAATC GCTTGGTCCC	360
CGGGAGGGAG AGGTTGNTNG TGNAGCTGAG ATCACGCCAC TNGCACTCCA GGCTGGGNAA	420
CAAAAGGGAG ACCTTTNCTC AAAAAAAAT NAAAAATAAA AGTGATGAGT AGGATTGGGA	480
CCCNAGACAT CTTTCTCCA AGACC	505

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGCAGNCTC AAACCCTTGT CCTGGGATCA AACAATCCTC CCACCTCAGC CTTCAAAGTA	60
---	----

GATAGAACTA CAGGCATGCA CTACCATGCC TAATTTTTTA AAAAAAATT TTTTTTCAGA	120
GATGAGATCT CACTGTGTTT CCCAGGNTTG TCCGGAATC CTGGACTCAA GCGATCCTCC	180
CACCTTGGGC TGCCAAAGTG TTGGGATTAC AGGCATGAGC CACCATGCCT GGCCATACAC	240
TTTTTTTTTT TTTTAAANCA AGACGGAGTC TNGTTCCTGTC GCCCAGACTG GAGTGCAGGG	300
GCGTNATCT TGGCTCACTT GAAAGCTTCG CCTCCCAGGG TTCATGCCGT TCTCCTGNCT	360
CAGCTCCCA AGTNGGTGGG ACTACAGGNA TCTGCACCAC GNCCGGTTAT TTNTTGGGTT	420
TGNNGNAGGG ACGGGGTTTC ACCATGTAG GCAGGATGAC TTCGGACTTC CNGACCCAAG	480
ATCACCTGC TCGGCTCCCA	500

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCCAGA CGAGCCTGGG CAACACAGTG AGACTCTATC ACTACAAAAA AATTTTAAAA	60
TTAGCTAAAG TTGATGGNAC ATGCCTGCAG TCCCAGCTAC TCAGGAGGCT GGGGCAGGAA	120
GATAGCTTGA GCCTGGGAGT TAGAGGCTGT GTGAGCTATG ATCACACTAC TGCACTCCAG	180
CCTGGGCAAC ACAGCAAGAC CCTAAACTA AAAAAGAAAA GAAAAAAAAA ATATATGTAC	240
GTNTTTGGGG AATTTCAAAG TGGGAGATAA ATCATTTTTC CAGACAGTNT CTTGAAACCC	300
AAAGTTTATG CTAAATAAA GGTGTGCTTT CTTTCACCTT CAAANGCGGG AGAAGGATCA	360
TCATNCACAC ACACACTN ATCATNCACA TTTTACAAA TNCAATTNNN NAATACAACA	420
CATTTTAACA TGGGGTTTTG	440

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCTGTT TCTTAAAACA GAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
TTGTATTAAA TGGATCATTT AATTTAATCT TCATAACTGA CATAGGAGTT GAGTAACTTG	120
TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGGCGC AGTGGCTCAA GCCTGTAATC	180
CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACCTGAGG TCAGGAGTTT GAGACCAGCC	240
TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GCGTGGTG	300
NTGCGCACTT GTAGTCCCAG CTACTCGGAA GGCTNGAGGC AGGAGGAATC GCTTGATCCC	360
NGGGAGGGAG AGGTTGGTNG TGANGCTGAG ATCACGNCAC TTGNACTCCA GNCTGGGNAA	420
CAAANGNGAG ATCTTNTCTC AAAAAAAAAAT AAAANTAAAA NGTGATGAGT AGGATTTGGA	480
CCCCAGACAT CCTNTCTCCA GGACCTGGNA TTC	513

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCCTGG NCTCAAGTGA TCCTCTCACC TCAGCCTCCC AAATTGCTGG GATTAGAGTG	60
TGAGCCACTG TGCCTAGCCT GCATATATCT ATTTTAAATG ACTGCTAAAT CTCATTGTAT	120
GAAAATTTAT GTCCTAGCTA TAAAATTTGN TAGCACATGT TTAATTTTTT CTAATTTTCTAG	180
ATGTTTTTAAA CTAATATTTT CCAAAGTATA GTATGGCATT TTAGGTATGA TATGATCTTT	240
NNTCCTCTTC GTACTCATTT TTATAGTTAT GGCCTGTGCA ACTGGTTTCC CATTTATATG	300
AATGATACAG AGCTTCCTAT TAAGAAAAAG TTCAGCTTGG GGAAAAAAA AGTGAATTGT	360
CAACTTNGAG GGAAAAAAGT GAATTATTGG	390

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTTC	60
AAACCCAAGA CTGATAATTT GTTTGTGACA GGAATGCCCC ACTGGAGTGT TTTCTTTCCT	120
CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC ATCCCATAAC TCTTCAGTAA	180
ATCATTAAAT AGCTATAGTA ACTTTTTTCAT TTGAAGATTT CGGCTGGGCA TGGTAGCTCA	240
TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG ATCACCTAAG CCCAGAGTTC	300
AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA GAAAATACAA AAATTNGNCG	360
GGNATG	366

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AACACCAGGG NCATGAGGGC ACTAATCATA ATGAGATATG CCTGCTGGAG TCGAAGTGGA	60
CCTTTCCAGT GAATGGAAAT CATTCACCAC ACACCAAAT TCCAGATCAG GAGTGNAACA	120
GTAATGTAGT CCACAGCAAC GTTATAGGTT TTAAACACTT CCCTGAAAAA AAATTACACA	180
GATTTTAAAA GATGTACAAT AATTTCCACC AAAACATTAT TTAGAATAAT GTGATGGCTC	240
CCAAACATTA GATATTAATN TCCCACCTTT ATAATTTTAC CATAACCTAT ATCAACTGTG	300
CTATTATTTA TTTAATNCTT CCCTNTAAAT TAATTTACTC TTTTTTTGTT TTTGTTTTTG	360
NGTTTGGAGC CAGTGTCTCA TTTTGGTTGC CCAGGCTTGG AGTAAAGTGG GTGCAATCAC	420
GGCTCAACTG NAGTCTTTNC CTCNNGGAGA TCAGGTNGGT CTTCCCCAGG TCCAANCTCC	480
TAAGTTGGTT NGGANAAC	498

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAAACAACAG	GGNCATGAGG	GCACTAATCA	TAATGAGATA	TGCCTGCTGG	AGTCGAAGTG	60
GACCTTTCCA	GTGAATGGAA	ATCATTTCCA	CCACACCAAA	ATTCCAGATC	AGGAGTGAAA	120
CAGTAATGTA	GTCCACAGCA	ACGTTATAGG	TTTTAAACAC	TTCCCTGAAA	AAAAATTACA	180
CAGATTTTAA	AAGATGTACA	ATAATTTCCA	CCAAAACATT	ATTTAGAATA	ATGTGATGGC	240
TCCCAAACAT	TAGATATTAA	TNTCCCACCT	TTATAATTTT	ACCATAACCT	ATATCAACTG	300
TGCTATTATT	TATTTAATNC	TTCCCTCTAA	ATTAATTTAC	TCTTTTTTTG	TTTTTGTTTT	360
TGTGTTTGGA	GCCAGTGTCT	CATTTTGGTT	GCCCAGGCTT	GGAGTAAAGT	GGGTGCAATC	420
ACGGCTCAAC	TGNAGTCTTT	ACCTCCCGGA	GATCANGTTG	GTCTTTCCC		469

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTTATCAAG	TACCTCCCTG	AATGGACTGN	GTGGCTCATC	TTGGCTGTGA	TTTCAGTATA	60
TGGTAAAACC	CAAGACTGAT	AATTTGTTTG	TCACAGGAAT	GCCCCACTGG	AGTGTTTTCT	120
TTCTCATCT	CTTTATCTTG	ATTTAGAGAA	AATGGTAACG	TGTACATCCC	ATAACTCTTC	180
AGTAAATCAT	TAATTAGCTA	TAGTAACTTT	TTCATTTGAA	GATTTCGGCT	GGGCATGGTA	240
GCTCATGCCT	GTAATCTTAG	CACTTTGGGA	GGCTGAGGCG	GGCAGATCAC	CTAAGCCCAG	300
AGTTCAAGAC	CAGCCTGGGC	AACATGGCAA	AACCTCGTAT	CTACAGAAAA	TACAAAAATT	360
AGCCNGGNAT						370

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCATGGTGT TGGCGGGGAG TGTCTTTTATG CATGCTAATG TATTATAATT AGCGTATAGT	60
GAGCAGTGAG GATAACCAGA GGTCACTCTC CTCACCATCT TGGTTTTTGGT GGGTTTTTGGC	120
CAGCTTCTTT ATTGCAACCA GTTTTATCAG CAAGATCTTT ATGAGCTGTA TCTTGTGCTG	180
ACTTCCTATC TCATCCCGNA ACTAAGAGTA CCTAACCTCC TGNAAATTGA AGNCCAGNAG	240
GTCTTGCCCT TATTTNACCC AGCCCCTATT CAAATAGAG TNGTTCTTGG NCCAAACGCC	300
CCTGACACAA GGATTT	316

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGCAGNCCG GGGGATCCTG GTAAAAGTCA CAAGGTCAGC CTACTAAAGC AGGGAAAAC	60
AAAGGCAAGT AAACACGTGC AGACAAAAA AGGGATAAAG AAAAGGAATT AAGAAACTAG	120
CATTTTAAAN GTGGGGGAGG TGAATGCTTC CCAGAATGGG TTTATATCAC TTGCTTGNGG	180
GCCTTCTGAG TGTGNAAC AACCTGTCAT CATCACACAT ACCTGTCATC TTTAATGGTC	240
TCCATACATT ACTAATAGAT TATACAGATG GCCATCACTT AACACTTCCA CTCACTCAAT	300
TTGTNCAACA TGCAAGGTTA CCCTCTTTTT TNGCTTACNG CCACAAAGCA TTGGANAAGG	360
TTTGTGATTT TTACTAGCCN CCACTTCATC AAATTTAAGC ATTTTCTTTT TCCTNTTAAC	420
ANCCAGGACA GGNTTNAACN AAGGAAAT	448

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGCAGCTCC AAGCACCTTT TTCAAATTCA GCTTTCTGTG ATTTTCAGACC ACATATGCAA	60
GGAACTATCT TACCTTAATT AATAAGACTT TAAATCCTT GTGTCAGAGG CGTTTGGACC	120
AGAGCAACTC TATCTTGAAT AGGGGCTGGG TAAAATAAGG CCAAGACCTA CTGGGCTGCA	180
TTTGCAGGAG GTTAGGTACT CTTAGTTACG GGATGAGATA GGAAGTCAGC ACAAGATACA	240
GCTCATAAAG GATCTTGCTG ATAAACTGG TTGCAATAAA GAAGCTGGNC AAAACCCACC	300
AAAACCAAGA TGGTGAGGAG AGTGACCTCT GGTATCCTC ACTGNTCACT ATACGNTAAT	360
TATTATACAT TAGCATGCTA AAAGACACTC CCCGCAACAA CCATGANAGG TTTACAAGTT	420
NCCATGGNAA CGNNCCCGGA NGNTANCTTG	450

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGNAGCCTC CACCACCCAG GTTCAGGTGA TTCTCCTGCC GTAGNCTCAT GAGTAGNTGG	60
GATTACAGGC ATGTGCCACC ATGCCCGACT AATTTTTATA TTTTGTAGTAG AGACGGGGTT	120
TCACCATGTT GGGCAGGCTG GTCTCAAACCT CCTGACCTCA AGTGATCTGC CCACCTTGGC	180
CTCCCAAAGT GCTGGGATTT CAGGCGCCTG GCCTGTTACT TGATTATATG CTAAACAAGG	240
GGTGGATTAT TCATGAGTTT TCTGGGAAAG AGGTGGGCAA TTCCCGGAAC TGAGGGATCC	300
CTCCCCTTNN NAGACCATAC AAGGTAACCT CCGGACGTTG GCATGGNATC TTGTTAAACT	360
TGTCATGGNG TTGGGGGGGA GTGTCTTT	388

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGCAGAAGT ATGTTTCCTG TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA	60
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ACACATAAAT TCTTTTCCAC CTCAGGGNCA TTGGGCGCCC ATTGCTCTTC TGCCTAGAAT	120
ATTCTTTTCTT TTTCTAACTT TGGTGGATTA AATTCCTGTC ATCCCCCTCC TCTTGGTGTT	180
ATATATAAAG TNTTGGTGCC GCAAAAGAAG TAGCACTCGA ATATAAAATT TTCCTTTTAA	240
TTCTCAGCAA GGNAAGTTAC TTCTATATAG AAGGGTGAC CCNTACAGAT GGAACAATGG	300
CAAGCGCACA TTTGGGACAA GGGAGGGGAA AGGGTTCTTA TCCCTGACAC ACGTGGTCCC	360
NGCTGNTGTG TNCTNCCCCC ACTGANTAGG GTTAGACTGG ACAGGCTTAA ACTAATTCCA	420
ATTGGNTAAT TTAAAGAGAA TNATGGGGTG AATGCTTTGG GAGGAGTCAA GGAAGAGNAG	480
GTAGNAGGTA ACTTGAATGA	500

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTGCAGAGTA ATTGCAACTG GAGTTGTCTT AAGATAATGT CACATATCCA TCTTCCCCTT	60
GTTTCTCATT CACAGAAAAA CATTTTTTATT CCAGGTGCCA ATATTCCCAG CCAAAAAGAC	120
TTTACTTCTG ACTCCCTTAT ATTTAGGATG GCTATGAGAA CAAGTAAGGG CAATGACTTC	180
TAGGGAGATG TGTGTGTAT GGAACCTCTA AGGAGAGAAT TCTGCTGACA TGTCCTATGT	240
TCTTTTCTCC CCTACTCCTT CCTACTGTCA GAAATGAAGG CTAGGGCTCC AGCCTGGACC	300
CTGAAGTAAG CTAGAGGTTA GAAGCTAAAG AAGAAAGAAG GAGATTGAGT CCTTGGATGA	360
ACGTGAAGCC ACCCTACTAA TCTGGACTGN CTACCTCTGN ACTACTCTAT GAGAGAGAAA	420
GTATGTGCAT TATTT	435

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATGCTCTTT GTCCCTGTGA CTCTCTGCAT GGTGGTGGTC GTGGNTACCA TTAAGTCAGT	60
CAGCTTTTAT ACCCGGAAGG ATGGGCAGCT GTACGTATGA GTTTGGTTTT ATTATTCTCA	120
AAGCCAGTGT GGCTTTTCTT TACAGCATGT CATCATCACC TTGAAGGCCT CTGCATTGAA	180
GGGGCATGAC TTAGCTGGAG AGCCCATCCT CTGTGATGGT CAGGAGCAGT TGAGAGAGCG	240
AGGGGTATT ACTTCATGTT TTAAGTGGAG AAAAGGAACA CTGCAGAAGT ATGTTTCCTG	300
TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA ACACATAAAT TCTTTTCCAC	360
CTCAGGGGCA TTGGGCGCCC ATTGNTCTTC TGCCTAGAAT ATTCTTTCCT TTNCTNACTT	420
GGGNGGATTA AATTCCTGT	439

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCCATCTCTA CGACTCTCAT GGGGTCCAAA GAAGAGTTTT AATTGAGTTT TAGAATGTGN	60
AGTTGTGAAG TGTCTGAAAA ACTACATGGT GNTCTGAAAG NCAAACTTTT AGCCTTGGGG	120
GAGAGCATCT AAGACAGNAG GTGAAGGGGA GGGGTTAGAN CTAGAGGGAT TGAAGAATAT	180
TATCCATATA GGTTAGGGTT AGGTGTGGCA ACGTTTTATA GAACAAACAT TGGNAAGCTA	240
CAGACACAGG CCAGNTCTGT CTNCTACCTN TCCACAAAGG TGTNATAACA AAGTTANNCA	300
CAAATGTGTG AATAAACT	318

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG	60
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AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT	120
AATAGTGCTT TTTCNTTTTT TTTTTTTNTT TTTTTTNNTT TTNGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTTGGG NTTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGCAGNTGA GCCGTGATTG CANCCACTTT ACTCCNAGCC TGGGCAANCA AAATGAGACA	60
CTGGCTNCAA ACACAAAAAC AAAAACAAAA AAAGAGTAAA TTAATTTAAA GGGAAGTATT	120
AAATAAATAA TAGCACAGTT GATATAGGTT ATGGTAAAAT TATAAAGGTG GGATATTAAT	180
ATCTAATGTT TGGGAGCCAT CACATTATTC TAAATAATGT TTTGGTGGAA ATTATTGTAC	240
ATCTTTTAAA ATCTGTGTAA TTTTTTTTCA GGGAAGTGTT TAAAACCTAT AACGTTGCTG	300
TGGACTACAT TACTGTTGCA CTCCTGATCT GGAATTTTGG TGTGGTGGGA ATGATTTCCA	360
TTCACTGGAA AGGTCCACTT CGACTCCAGC AGGCATATCT CATTATGATT AGTGCCCTCA	420
TGGCCCTGGT GTTTATCAAG TACCNCCCTG AATGGACTGG GTGGCTCATC TTGGCTGTGA	480
TTTCAGTAT	489

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGCAGNCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCACC ATGCCCGGCT AATTTTTGTA TTTTCTGTAG ATACGAGGTT	120
TTGCCATGTT GCCCAGGCTG GTCTTGAAC TGGGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA	240
AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCCTGTGA	360
CAAACAAATT ATCAGTCTTG GGTTTTACNA TATACTGAAA TCACAGCCAA GATGAGCCAC	420
GCAGTCCATT CAGGGAGGTA CTTGATAAA	449

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGCCGT TCCCGACCCG AGCCTGGTGC CCCTTCCCCA TTATGATCCT TNTCGCTTCC	60
GGCGGCATCG GGATGCCCCG CGTTGCAGGC CATNCTGTCC CAGNCAGGTA GATGACGACC	120
ATCAGGGACA GCTTCAAGGA TCGCTCGCGG CTCTTACCAG CCTAACTTCG ATCATTGGAC	180
CGCTGATCGT CACGGCGATT TATCCCGCCT CGGCGAGCAC ATGGAACGGG TTGGCATGGA	240
TTGTAGGCGC CGCCCTATAC CTTGTCTGCC TCCCCGCGT TGCCTCGCGG TGCATGGAGC	300
CGGNCCACCT CGACCTGAAT GGAANCCGGC GGCACCTCGC TAACGGATTG ACCACTCCAA	360
GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC NCAAAACCAAC CCTTGGCAGA	420
ACATATCCAT CGCGTCCGCC ATCTCCANCA GCCGCACGCG GCGCATCTCG GGCAGCGTTG	480
GGTCCTGCAG	490

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGCAGTGTT TAAAAAATAA AATAAACTAA AAGTTTATTT ATGAGGAGTA CACTGCTTTC	60
TTGTAAACAC ATGTACAAGC CATATAATAG AGTTCATTTT NNACCCTAGT TACGGAAACA	120
CTAGAAAGTC TNCACCCGGC CAAGATAACA CATCTTTAGG TAAAAATAGC AAGAAATATT	180
TTATGGGTTG TTTACTTAAA TCATAGTTTT CAGGTTGGGC ACAGTGGNTC ATGCCTGTAA	240
TCCCAGCACT TTATGCGGCT GAGGCAGGCA GATCAGTTGA GGTCAGAAGT TTGAGACCAG	300
CCTGGGCAAT GTGGCAAAAC CTCATCTCCA CTAAAAATAC AAAAATTAGC CAGGCATGGT	360
GGTGACACA TGTTAATTCC CAGCTACTTG GGAGGNTTGA GACAGGAGGG TCGCTTGGNC	420
CTAGGAGGGA AGAAGTTGNA GGGANCTTAA TGTCAC TGCA CTCTAGNTTG	470

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CACTCAATTC TGAATGCTGC CATCATGATC AGTGTCATTG TTGTCATGAC TANNCTCCTG	60
GTGGTTCTGT ATAAATACAG GTGCTATAAG GTGAGCATGA GACACAGATC TTTGNTTTC	120
ACCCTGTTCT TCTTATGGTT GGGTATTCTT GTCACAGTAA CTTAACTGAT CTAGGAAAGA	180
AAAAATGTTT TGTCTTCTAG AGATAAGTTA ATTTTTAGTT TTCTTCCTCC TCACTGTGGA	240
ACATTCAAAA AATACAAAAA GGAAGCCAGG TGCATGTGTA ATGCCAGGCT CAGAGGCTGA	300
GGCAGGAGGA TCGCTTGGGC CCAGGAGTTC ACAAGCAGCT TGGGCAACGT AGCAAGACCC	360
TGCCTCTATT AAAGAAAACA AAAAACAAAT ATTGGAAGTA TTTTATATGC ATGGAATCTA	420
TATGTCATGA AAAAATTAGT GTAAA	445

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CCTGTATTTA TACTGAACCA CCAGGAGGAT AGTCATGACT ACAATGACNC TGATCATGAT	60
GGCAGCATTG AGAATTGAGT GCAGGGCTCT CTGGCCCACA GTCTCGGTAT CTTCTGTGAA	120
TGGGGTATAG ATTCTACAAT AAAACAAACA CAAAAGCCCT AGGTCAGTGT TAATGGAGAT	180
CACCAACCAC ATTACCACCT CCAACACAGA ATTTTCTTTT TCTTAATTCA ATTCGNATCT	240
TATAAGTCAC TTTTCCCCAA CTCACCAATN CTAGCTAAGA ATTTTTAACC TGAGAAAAAC	300
AGCTACACTC TAAAATTGCT TCAAAGAAAA TGTCTAACAT ATGGAAAGAA GGACTTAACA	360
TGTGAAGCAG ACACTGGCTC CATCTAGTGG GTGCTTTATA TTGAAATAAT TATAATACCT	420
CATCAAATTT TTTNGGGTAC AGNTTATTAG GAACTTGGTA TGGAACCAGA TTCTGCCACA	480
GAAACCACGN GGGCTG	496

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATTAGATAA TGGNTCAGGG TGGCCAAGGC TCCGTCTGTC GTTGTGCTCC TGCCGTTCTC	60
TATTGTCATT CTATAAGCAC AAGAAAAACA TTTTCAGTAA ATCAGATTCT CAGCAGAATC	120
AAGGTAACGG TTAGACCTGG GATTAACAAC AGACCCGTCA CTATGAGTTC TAAAAACCTG	180
AAGCAAGAAA AAACAATGTA CAGGAAGTAT GCAGTTTAAA AGTCTAGATT ATCTATCATT	240
GTTCACTGAA GGCATTTCAGG TCCTCTCTTT TACCTGGGTC TTGGNTTGCT CCATTCTCTC	300
TGTTTCATCCC AACATACACA ATTGTACTTA TCCTTTGAGA TGTACCTTAA ATACTGACAC	360
CTGCATGAAA ACTTGTTTAC TGGCTGCAGG TCCAAGCACC TTTTTCNAAA TTCAGCTTTC	420
TGTGATTTCA GACCACATAT GCAAGGAACT ATCTTACCTT AATTAATAAG ANTTTAAAT	480

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AGGANCGCTT GGGCCCAGGA GTTCACAAGC AGCTTGGGCA ACGTAGCAAG ACCCTGCCTC	60
TATTAAAGAA AACAAAAAAC AAATATTGGA AGTATTTTAT ATGCATGGAA TCTATATGTC	120
ATGAAAAAAT TAGTGTAATA TATATATATT ATGATTAGNT ATCAAGATTT AGTGATAATT	180
TATGTTATNN NGGGATTTC AATGCCTTTTT AGGCCATTGT CTCAAAAAAT AAAAGCAGAA	240
AACAAAAAAA GTTGTAAC TG AAAAATAAAC ATTTCCATAT AATAGCACAA TCTAAGTGGG	300
TTTTTGNTTG TTTGTTTGNT TGTGAAGCA GGGCCTTGCC CTNCCACCCA GGNTGGAGTG	360
AAGTGCAG	368

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCCTTT TTTTTTTTTT TTTTTTTTTT TTNCTCCTAA TGTTTTTATT GTNCCTTAGA	60
TAACTGGATA GNACAAAGTT NGNCTTNGTT TTTTACTTAA AAAACGTACT TTCCGCATAC	120
TGTNGCCCGT ATGACTTTCC TGTCCCATCG GAAACCAGAG TTTCCCAGG TGAGCCCTTC	180
CTATCTGNGG NTACATGATT TAGCTAATTT AACAAGAAGA GAGTAATTCC TTNGGATTAT	240
TATCAACATG AAACCTGGAC TATGTCTCTA TAAGGGTGAA CACTGATTTT TTTTTTCTTT	300
TTAGAAACAA AAACCATCCA CTTATTAATC CAACTACGG GATTGGATTT ACAACAATCA	360
TCGCATNAAC TGAACATACG AAGTTACCAC TCAAGGGAAT NACAGAAGAA CGTTGNACAA	420
TNTNTCTTAC GGGGTACGNG AATTCAAACA ATGTGGGGAN AGGAACTTCA NTCTACAAAN	480

TCTGACCATC GNTTCAGTAT

500

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCCTTT ACTCTTCTTT AATTCTACCG TCTTTGGGCA TACATCTCAT TTGNTGTGGA	60
AGAAGGTCTG ACAGNAGGGC TGACAGCACC GATTCATAAC ACATTCTTTT CATCATACAA	120
AGAGTAAGAC CCTAGAATAA TGGGACCATC TGCTACCACG ACAGAGCTGC CTTACTGGCT	180
GTAGAAAAAG ACTGCTTGTG TGGGAGAGAA GAATGAGGAC AGAGGAGGCA TCTGGGGCAA	240
GTGAGCGTAC AAGTATNTCT ACAAATTCAG AATTTGGTGG AAAATCCAA TTTGNCTTCA	300
ACATGATAGA GAATTGATGA GAAAATAGCT GTNCTGTTTC CAAAATTTAC TGAATTTGGG	360
AACCTGAGGT TAAAACTTTT AGGATNAAGC AACTCAGGTT CAAGACTTNG NCTNGGGAAG	420
GAATGGAAAC ACAGACGGGA ATGAGTNTCA	450

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAACTGTATT TATACAGNAA CCACCAGGAG GATAGTCATG ACAACAATGA CAACTAGGA	60
ATAGCCCCCT TTTACTTCTG AGTCCCAGAG GTTACCCAAG GCACCCCTCT GACATCCGGC	120
CTGCTTCTTC TCACATGANA AAACTAGCC CCCAGTNTGA TCCGCAGGTN GAGGAATNCC	180
CCGGGTCGAG GTTCGGATCC TGGATGACAG ACCCTCTCGC CCCTGAAGGN GATAACCGGG	240
TGTGGTACAT GGACGGNTAT CACAACAACC GCTTCGNACG TGAGTACAAG TCCATGGTTG	300
ACTTCATGAA CACGGACAAT TTCACCTCCC ACCGTCTCCC CCACCCCTGG TCGGGCACGG	360

GGNAGGTGGT CTNCAACGGT TCTTTCTNCT TCAACAAGTT CCAGAGCCAC ATCATCATCA 420

GGTTTGGACC TGAAGANAGA GAACATCCTC 450

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGATCCCTCC CCTTTTTAGTA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA 60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA 120
TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT 180
TGGCCAGCTT CTTTATTGCA ACCAGTTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT 240
GCTGACTTCC TATCTCATCC CGTAACTAAG AGTACCTAAC CTCCTGCAAA TNGCAGCCCA 300
GTAGGTCTTG GNCTTATTTT ACCCAGCCCC TATTCAAGAT AGAGTTGCTC NTGGTCCAAA 360
CGCCTCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGGT CCTTGGATAT 420
GTGGTCTGAA ATCACAGAAA GCTGAATTG GAAAAAGGTG CTTGGAGCTG CAGCCAGTAA 480
ACAAGTTTTC ATGCAGGTGT 500

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGCAGTGAG CCAAAATCGT GCCACTGCAC TTCACTCCAG CCTGGGTGAC AGGGCAAGGC 60
CCTGCTTCAA CAAACAAACA AACAAACAAA AACCCACTTA GATTGTGCTA TTATATGGAA 120
ATGTTTATTT TTCAGTTACA ACTTTTTTTG TTTTCTGCTT TTATTTGTTG AGACAATGGC 180
CTAAAAAGGC ATTGAAATNC CAAAATAACA TAAATTATCA CTAAATCTTG ATAATAATC 240
ATAATATATA TATTTTACAC TAATTTTTTC ATGACATATA GATTCCATGC ATATAAAATA 300
CTTCCAATAT TTGTTTTTTG TTTTCTTTAA TAGAGGCAGG GTCTTGCTAC GTTGCCCAAG 360

CTGCTTGTGA ACTCCTGGGC CCAAGCGATC CTCCTGCCTC AGCCTCTGAG CCTGGCATT	420
CACATGCACC TGGCTTCCTT TTTGTNTTTT TTGAATGTTT CACAGTGAGG AGGAAGAAAA	480
CTNAAAATTA ACTTATCTCT	500

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGCAGATGA GAGGCACTAA TTATAAGCCA TATTACCTTT CTTCTGACAA CCACTTGTCA	60
GCCCACGTGG TTTCTGTGGC AGAATCTGGT TCTATAACAA GTTCCTAATA AGCTGTAGCC	120
AAAAAAATTT GATGAGGTAT TATAATTATT TCAATATAAA GCACCCACTA GATGGAGCCA	180
GTGTCTGCTT CACATGTTAA GTCCTTCTTT CCATATGTTA GACATTTTCT TTGAAGCAAT	240
TTTAGAGTGT AGCTGTTTTT CTCAGGTAA AAATTCTTAG CTAGGATTGG TGAGTTGGGG	300
AAAAGTGA CT TATAAGATAC GAATTGAATT AAGAAAAAGA AAATTCTGTG TTGGAGGTGG	360
TAATGTGGGT GGTGATCTTC ATTAACACTG ANCTAGGGNT TTGGGGTTTG GTTTATTGTA	420
GAATCTATAC CCCATTCANA GAAGATACCG	450

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCAGCCAG TAAACAAGTT TTCATGCAGG TGTCAGTATT TAAGGTACAT CTCAAAGGAT	60
AAGTACAATT GTGTATGTTG GGATGAACAG AGAGAATGGA GCAAGCCAAG ACCCAGGTAA	120
AAGAGAGGAC CTGAATGCCT TCAGTGAACA ATGATAGATA ATCTAGACTT TTAAACTGCA	180
TACTTCCTGT ACATTGTTTT TTCTTGCTTC AGGTTTTTAG AACTCATAGT GACGGGTCTG	240

TTGTTAATCC CAGGTCTAAC CGTTACCTTG ATTCTGCTGA GAATCTGATT TACTGAAAAT	300
GTTTTTCTTG TGCTTATAGA ATGACAATAG AGAACGGCAG GAGCACAACG ACAGACGGAG	360
CCTTGCCAC CCTGAGCCAT TATCTAATGG ACGACCCAGG GTAACCTCCG GCAGGTGGTG	420
GAGCAAGATG AGGAAGAAGA TGAGGAGCTG ACATTGAAAT ATGGCGGCNA GCATGTGATC	480
ATGCTCNTTG GCCCTGTGAN TC	502

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCAGTGTT CCTTTTCTCC ACTTAAAACA TGAAGTAATA ACCCCTCGNT CTCTCAACTG	60
CTCCTGACCA TCACAGAGGA TGGGCTCTCC AGCTAAGTCA TGCCCCTTCA ATGNAGAGGC	120
CTTCAAGGTG ATGATGACAT GCTGTAAAGA AAAGCCACAC TGGGTTTGAG AATAATAAAA	180
CAAACTCAT ACGTACAGCT GCCCATCCTT CCGGGTATAA AAGCTGACTG ACTTAATGGT	240
AGCCACGACC ACCACCATGC AGAGAGTCAC AGGGACAAAG AGCATGATCA CATGCTTGGC	300
GNCATATTTT AATGTCAGNT CCTCATCTTC TTCCTCATCT TGNTCCACCA CCTGCCGGGA	360
GTTACNTGG GTCGTCCATT AGATAATGGG TCAGGGTGGC CAAGGCTCCG TCTGTCGTTG	420
TGCTCCTGCC GTTCTCTATT GTCATTCTAT AAGCACAAGA AAAACATTTN CAGTAAATCA	480
GATNCTCAGC AGAATCAAG	499

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TAACTCCCAG GNTCAAGATN TCTNCCTGCG TTAGCCTCCT GAGTAGCTGG GACTATAGGT	60
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ATGTGCCACT ATTCCTGAAA ACATAATCAG TTTTGAAGGT AGTGTCTGGG CTGGGCGCAG	120
TGGNTCACGC CTTCAATCCC AGCACTTTGG GAGGNCGAGG TGGGCGGATC ACCTGAGGTC	180
AGGAGTTCGA GACCAGCCTG ACCAACATGG GATAAGACTC CATCTCTACT AAAAATACAA	240
AAAATTAGCC AGGCATGGTG GNGCATGCCT GTAATCCCAG CTACTCAGGA GGNTGAGGNA	300
GGAGAATTGG TTGGAACCTA GGAAGCAGAG GCTGTGGTGG AGCCGAGATC GCACCATTGG	360
ACTCCAGGCT GGGNAACAAG AGTGAAAATC CNTCTTAAAA AAAAAAAAAA AAAGGTAGNG	420
TTTTGNCCGG NGCGGGGGGT CACGCCTGTA ATCCCAGNAT TGGGGANGGC AAGNGGGGGG	480
GTCANNANGN NAGNAGTCCG	500

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCTGCT GACATGTCCT ATGTTCTTTT CTCCCCTACT CCTTCCTACT GTCAGNAATG	60
AAGGGTAGGG CTCCAGCCTG GACCTGAAG TAAGCTAGAG GTTAGAAGCT AAAGAAGAAA	120
GAAGGAGATT GAGTCCTTNG ATGAACGTGA AGCCACCGTA CTAATCTGGA CTGCCTACCT	180
CTGCACTACT CTATGAGAGA GAAAGTATGT GCATTATTTA AACCAGTTGG GTTGATTTTC	240
TATTAACAAA GTCAGAAACA TCTCTGTAAA AAGCCAGACT GAATATTTTA AGCTCTATGG	300
GTCATATGGT CTCCAGGGCA AACACTCAAC TGTGCTACTG TAGTGTGAAA GCAGGCACAG	360
ACAATGTATT AACCAAGGAG GGTGGTCACT TTCCAATGAA AGTTTATCAC AAATTGGNGA	420
ATACTTG GTA TTACACCNG GGGGAAGGTA GGAGAAGATC TTGCCTGTGG TTGTNGNTGG	480
CAATGTTGGT CTTTATACG NG	502

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCTCTC CTTAGAAGTT CCATACACAA CACATCTCCC TAGAAGTCAT TGCCCTTACT	60
TGTTCTCATA GCCATCCTAA ATATAAGGGA GTCAGAAGTA AAGTCTGGNT GGCTGGGAAT	120
ATTGGCACCT GGAATAAAAA TGTTTTTCTG TGAATGAGAA ACAAGGGGAA GATGGATATG	180
TGACATTATC TTAAGACAAC TCCAGTTGCA ATTACTCTGC AGATGAGAGG CACTAATTAT	240
AAGCCATATT ACCTTTCTTC TGACAACCAC TTGTCAGCCC ACGTGGTTTC TGTGGCAGAA	300
TCTGGTTCTA TAACAAGTTC CTAATAAGCT GTAGCCAAAA AAATTTGATG AGGTATTATA	360
ATTATTTCAA TATAAAGCAC CCACTAGATG GAGCCAGTGT CTGCTTCACA TGTTAAGTCC	420
TTCTTTCCAT ATGTTAGACA TTTCTTTGAA GCAATTTTAG AGTGTAGCTG TTTCTCAGGT	480
TAAAATTCTT AGTAG	495

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TATGGTTGCC TATTCTTGTC ACAGTAACTN AACTGATCTA GGAAAGAAAA AATGTTTTGT	60
CTTCTAGAGA TAAGTTAATT TTTAGTTTTT TCCTCCTCA CTGTGGAACA TTCAAAAAAT	120
ACAAAAAGGA AGCCAGGTGC ATGTGTAATG CCAGGCTCAG AGGCTGAGGC AGGAGGATCG	180
CTTGGGCCCCA GGAGTTCACA AGCAGCTTGG GCAACGTAGC AAGACCCTGC CTCTATTAAA	240
GAAAACAAAA AACAAATATT GGAAGTATTT TATATGCATG GAATCTATAT GTCATGAAAA	300
AATTAGTGTA AAATATATAT ATTATGATTA GTTATCAAGA TTTAGTGATA ATTTATGTTA	360
TTTTGGGATT TCAATGCCTT TTTAGGCCAT TGTCTCAAAA AAATAAAAGC AGGAAAACAA	420
AAAAAGTTGT AACTTGAAAA ATAAACATTT CCATATTTAT AGCCAACTAA GTGGGTTTNG	480
GGTNGGTTGG GTTGGTTGGT	500

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TTATCATTA	AAGGTCCCAC	AACCCCTAAA	AAGTACAGAT	TTTTTTTTTC	TTNGTGGAGA	60
CAGGGTCTCA	CTTGGTCGCC	CAGACTGGAG	TGCAGTGGCA	CGATCTCAGT	TCACCACAAC	120
CTCTGCCTCC	TGGGTTCAAG	CAATNCTCGT	GCTTAAGCCT	CCTGAGTAGG	TGGAACCACG	180
CGTGCGCGCC	ACCACGCTAG	GTTNATTGTG	GCTTTTTTAG	TAGAGACAGG	GTTTCGCCAT	240
GTTGCCCAGG	CTGGTCTCAN	ATTCCNGACC	TCAAGTGATC	CGNCCGCCTC	AGACTCCCAA	300
AGTGNTGAGC	ATTACAGNTG	TGTACCACTA	TGTCCCNGNC	CNCATCTCTC	TTTAAACAN	360
CTTNCATTTA	CCTAGTCCAC	TCCTG				385

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACCTAGAAA	AGAAAGCATT	TCAANNTAAT	TAACAGGTCC	CACAACCCTT	AAAAAGTACA	60
GATTTTTTTT	TTCTTTNNGG	AGACAGGGTC	TCACTTTGTC	GCCCAGACTG	GAGTGCAGTG	120
GCACGATCTC	AGCTCACCAC	ANCCTCTGCC	TCCTGGGTTC	AAGNANTTCT	CGTGCTTANG	180
CCTCCTGAGT	AGGTGGAACC	ACGCGTGTGC	GCCACCACGC	TAGGCTACTT	TNTGTATTTT	240
TAGTAGAGAC	AGGGTTTCGC	CATNTTGCCC	AGGCTGNTCT	CAAATTCCTG	ACCCNCAAGT	300
GATCCCCCCN	CCTTCAGTAC	TCCCCATCAG				330

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
GGTGGNCGTT CTAGAACTAG TGGCNCCCAA GGNAGAAGAA GTTTTCTTAG TACAGAACAA      60
AATGAAANGT CTCCCATGTC TACTTCTTTC TACACAGACA CGGCATCCAT CCGTTTTTCT      120
CANTCTTTCC NCCACCTTTC CCGTCTTCTT ATTCCACAAA GCCGNCATTG TCATCCTGGC      180
CCNTTCTCAA TGAGCTGTTG NNTACACCTC CCAGACGGCG TGGTGGNCGG TCAGAGGGGC      240
TCCTCACTTC CCAGTAGGGG TGGCCGNGCA GGNGGTGCCC CNCACCCCCC GGGCGGGGTG      300
GTTNGTCCNN CCGGNGGGNT GCACCNCCCC CACCCCTCCC CNCTCTNCTA CTGGCGGTCTG      360
TNTATTNCAN NATCTTTAAG CA                                             382
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
GGATCCAAAG GAAGTTAGAG GCCAGCTCAG TCTACACCTG CTACTGNTCA GTGCCCACCC      60
GGTCAAGGGA GACCAACACA TGGTAAAGGT CAAGGGCTTC TTGGAAGGCA GTCAGCAGCC      120
TGTGCAAGAT GTTCTCCACA CTGCTCAGNT TAAGGGGAGC TGGGGGCAGG ACCTCAGCTG      180
GNATCTCTGC TTCACCAGTG TCCAGGGGTT GCACAATTCT TGTTTACTCG TAGGATATTT      240
AATCTTGGNN GGTGCTATCA TAAATGGGAC TTATCCNCTN ATTATGTTTT CTTACTAGTT      300
GTTTATGTGA AGGTTATTGA TTTGGGTTTC ACTTTATTTN GTGGNAATGG AGTTTCACTC      360
```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AATGTCACGG ATTCCTTTAG GTAGNTACAC CCATCAACCT TTTTGAGAAT AAAATGAATT	60
GAGAGTGTTA CAGTCTAATT CTATATCACA TGTAACTTTT ATTTGGATAT ATCAGTAATA	120
GTGCTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GNGANAGAGT CTCGCTCTGT	180
CGCCAGGTTG GAGTGNAATG GTGCGATC	208

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AACAAGGTTT CTCGGTCGGC GGTGAATATA CCGGGGCGTC GATATTTGTT GCGGAATACT	60
CCCCTGACCG TAAACGTGGC TTTATGGGCA GCTGGCTGGA CTTCGGTTCT ATTGCCGGGT	120
TTGTGCTGGG TGCGGGCGTG GTGGTGTTAA TTTCGACCAT TGTCGGCGAA GCGAACTTCC	180
TCGATTGGGG CTGGCGTATT CCGTTCTTTA TCGCTCTGCC GTTAGGGATT ATCGGGCTTT	240
ACCTGCGCCA TGCGCTGGAA GAGACTCCGG CGTTCCAGCA GNATGTCGAT AAAGTGAAC	300
AGGGCGACCG TGAAGGTTTG GAGGATGGCC CGAAAGTCTC GTTTAAAGAG ATTGGCACTA	360
AATACTGGNG CAGNCTGTTG AATGTTTGGG CTTGGTAATT GGCAACCAAC GTGATTACTA	420
NATGTTGGTG ACCTATATTG CCGAGTTATT GGCGGATAAC CTGAATTATC	470

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TAATTATATT GAAATGCTTC TCNTCTAGGT CATCCATGNC TGGNTTATTA TATCATCTCT	60
ATTGNTGNTG CTCTTTTTTA CATNCATTTA CTTGGGGTAA GTTGTGAAAT TTGGGGTCTG	120
TCTTTCAGAA TTAACCTACCT NNGTGCTGTG TAGCTATCAT TTAAAGCCAT GTACTTTGNT	180
GATGAATTAC TCTGAAGTTT TAATTGTNTC CACATATAGG TCATACTTGG TATATAAAAG	240
ACTAGNCAGT ATTACTAATT GAGACATTCT TCTGTNGCTC CTNGCTTATA ATAAGTAGAA	300

CTGAAAGNAA CTTAAGACTA CAGTTAATTC TAAGCCTTTG GGGAAGGATT ATATAGCCTT	360
CTAGTAGGAA GTCTTGTGCN ATCAGAATGT TTNTAAAGAA AGGGTNTCAA GGAATNGTAT	420
AAANACCAAA AATAATTGAT	440

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AAAACAAAGC CTCTTGAGGT TCTGAAAAGG GAAAGAAAAA CAGAACTTTG TGCACTACAA	60
TTATACTGTT ATAAAAACA CTTCCATAGA TTACATTAAG CAGAAACAAA CCTTTCTTTC	120
ATGTGTTCTC CTCCAGGCCA AGCTGTCTAA GGACCGCAAA GGCTGTTGTC ACTTGCAGGC	180
TCCCAGATTA GGTCTGAAAT AGGATTTTAC CAGGTCATCC ATTGTTAGTT AAATCCTAGT	240
AAATTCATTT ANACCAATCA AATACTTATA AGACCAATTT GTAAACCAGG AATGTATTAA	300
TTTGTACAGA CTTTCAACTA ACTGACAAAT TTACTATAAG CTCAAGGTAG GACTCTTTAG	360
CAATAAGTAG GAACCGCCTG AGACAACCAA ACATTTTCAA CCCACAAANG ATACTTTAAT	420
GACTTTCTGA TTTNCCAGCA AAAGGGGGG	449

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGATCCGCCC TCCTCGGCCT CCCAAAGTGT TGGGATTACA GGCGTGAGCC ACCGCACCTG	60
GCTTTTTTTTT TTTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCCC AAGCTGGAGT	120
GCAGTGGTGC AATCTTG GTT CACTGNAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC	180
CTCAGTTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGC TAAATTTGGN	240
ATTTTTTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGGTCTT GAACTCCTGA	300

CCTTGTGATC CACCAGCCTC GGCCTCCCAA ATTGNTGGGA TTACAGGCGT GAGCCACCAC	360
AACCAGGCTA AAGTTTTTAAA ACATGCCAAG TGTATTTACA TAATGCGATA CGANTTATGT	420
ACATA	425

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNTTGTA AATAAGCATG TTATCTGTCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACA TTCCNTTAAG GATTACTCAA GCTCCCTTTG GTGTATATCA GNNGTCANNA	360
CNTATCTTNG GGGCTGAAAA ATGTTT	386

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAAAGGGAA AGAAAAACAG AACTTTGTGC ACTACAATTA TACTGTTATA AAAAACACTT	60
CCATAGATTA CATTAAGCAG AAACAAACCT TTCTTTCATG TGTTCTCCTC CAGGCCAAGC	120
TGTCTAAGGA CCGCAAAGGC TGTGTGCACT TGCAGGCTCC CAGATTAGGT CTGAAATAGG	180
ATTCACCAG GTCATCCATT GTTAGTTAAA TCCTAGTAAA TNCA	224

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGATCCGCCC TCCTCGGCCT CCCAAAGTGT TGGGATTACA GCGGTGAGCC ACCGCACCTG	60
GCTTTTTTTTT TTTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCCC AAGCTGGAGT	120
GCAGTGGTGC AATCTTGTT CACTGCAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC	180
CTCAGTTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGN TAAATTTGGG	240
ATTTTTTTTTT AGTAGAGACA GGGTTTCANC ATGTTGGCCA GGNTGGTCTT GGACTCCTGA	300
CCTGGTGAAC CACCAGGCTC GGGCTCCAAA TTTGGTTGGG ATTACAGGGG GTNAANCAAC	360
CACAACCCAG NCTAAAGTTT TNAAAACATN CAAAGTGTTT TAAAATNATG NGATACGATT	420
TATTGTACAA TTAATTTTAT	440

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTACTCCTTG CCATTTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA	180
TATTTGCGGN TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTTCTGTGT CCACATCTAA CAAAGTCAAG ATCCCCGGCT GGACTTTTGG	300
AGGTTCTTTC CAAGTCTTCC TGACCACCTT GCACTATTGG ACTTTGGNAA GGAGGTGCCT	360
ATAGAAAACG ATTTTGGAAC ATACTTCATC GCAGGGGGAC TGTGTCCCCC GGTGGCAGAA	420
NCTACCAAGA TTTGCGGGNC GAGGTCAA	448

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTTNAGTAA AATAAGNATG TTATCTGNCC GCCCTGCCTN	180
GGNNATTGNG ATAAGGAT	198

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGCAGTGAG CCGTGATTGC ACCACTTTAC TCCAGCCTGG GCAACAAAAT GAGACCCTGG	60
CTCAAAAACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTAAAGGGAA GTATTAAATA	120
AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGATA TTAATATCTA	180
ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTNTTGG TGAAAATTAT TGTACATCTT	240
TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT TGCTGTGGAC	300
TACATTACTG TTGCACTCCT GATCTGGAAT TTTGGGTGTG GTGGGAATGA TTTCCATTCA	360
CTGGAAAGGT CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCTCATGGNC	420
CTGGTGTTTA TCAAAGTACC TCCCTGAATG GACTGCGTGG GTCATCTTGG NTGTGATTCA	480
GTATATGGTA AAACCCAAGA	500

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTGCAGCCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCACC ATGCCCCGGCT AATNGNTGTA TTTTCTGTAG ATACGAGGTN	120
TNGCCATGTT GCCCAGGCTG GTCTTGAACCT CTGGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA	240
AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCCTGTNA	360
CAAAACAAAT TATCAGTCTT GGGGTTTNAC CATATACTGA AATCACAGGC AAGATGAGCC	420
ACGCAGTCCA TNCAGGGAGG TACTGGATAA CACCAGGGNC ATGAGGGACT AATCATAATG	480
AGATATGCTG CTGGAGTCGA	500

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 550 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGCAGGATG AGAGCGATCT CTTNTTNCAT TTCCTGCGCT ACGCGCTGCG GGCGACCAAA	60
TTCTTTCGCC ATAATAAATT CTCCTGACNA AAAAGGGGCT GTTAGCCCCT TTTTAAAATT	120
AATTTCAGGT GGAAGGGCTG TTCACGTTGA CCTGATAAGA CGCGCCAGCG TCACATCAGG	180
CAATCCATGC CGGATGCAGC GTAAACGCCT TATCCCGCAT GGAACCCTAA AAACCTTAAG	240
CAATGGTACG TTGGATCTCG ATGATTTCTGA ATACTTCGAT CACATCGNCA GTGCGGACGT	300
CGTTGTAGTT CTTAACGCCG ATACCACATT CCATACCGTT ACGGGACTTC GTTAACGTCA	360
TCTTTGGAAG CGGGGCAGGG ACTCCAGCTC GNCCTCGTAG ATAACCACGT TGGCACGCAG	420
GAACGCGGGT CGGGTTGTGA CGTTTAAACAC AACTTCCGGG TAACCATACA GGCTGNGATG	480
GNACCAAATT TCGGGGGATT TGGACAAGTC AAGAACTTCC CGCCAGACCG ATAATCTTGT	540
TGTTCAATTC	550

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTTA	120
TNTTGTTTAT GTTGCTCCCC CCACCCCCAC CAGTTCACCT GCCATTTATT TCATATTCAT	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTTCCT TCGTTAATTC	240
CTCCCTACCA CCCATTTACA AGTTTAGCCC ATACATTTTA TTAGATGTCT TTTATGTTTT	300
TCTTTTNCTA GATTTAGTGG CTGNGTTGTG TCCGAAAGGT CCACTTCGTA TTGCTGGTTG	360
AAACAGCTCA GGAGAGAAAT GAAACGCTTT TTCCAGCTCT CATTTACTCC TGTAAGTATT	420
TGGAGAATGA TATTGAATTA GTAATCAGNG TAGAATTTAT CGGGAACCTG AAGANATGTN	480
ACTATGGCAA TTTCANGGNA CTTGTCTCAT CTTAAATGAN AGNATCCCTG GACTCCTGNA	540
G	541

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

NNCCNCNCN NNNNNNNNTN NTNTTGCCCG ATAACATAG GGNGACTTGG AGATCCACCG	60
CGGTGGCGGN CGNTCTAGAA CTAGTGGATC CCCCAGGNTG CAGGACCCAA CGCTGCCCGA	120
GATGCGCCGC GTGCGGTTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT	180
GGTTTGC GCA TTCACAGTTC TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA	240
T	241

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
CCCCCCNCC NNNNNTTTTN NGCAGCCCGT AATTACCCTC ACTNCCGGGA ACAAAGCTG      60
GGTACCGGGC CCCCCCTCGA GGTCGACGGT ATCGATAAGC TTGATATCGA ATTCCTGCAG     120
TGTTTAAAAA ATAAAAATAAA CTAAAAGTTT ATTTATGAGG AGTACACTGC TTTCTTGTA      180
ACACATGTAC AAGCCATATA ATAGAGTTCA TTTTTTACCC TAGTTACGGA AACACTAGAA     240
AGTCTTCACC CGGCCAAGAT AACACATCTT TAGTAAAAAT AGCAAGAAAT ATTTTATGGG     300
TTGTTTACTT AAATCATAGT TTTCAGGTTG GGCACAGTGG NTCATGCCTG TAATCCCAGC     360
ACTTTATGCG GNTGAGGCAG GCAGATCAGT TGAGGTCAGA AGTTTGGAGA CCAGNCTGGG     420
CAATGTGGNA AAACCTCATC TCCACTAAAA ATACAAAAAT TAGNCAGGCA TGGTGGTGCA     480
CACATGTAAT TCCAGNTACT TGGGGAGGCT GAGACAGGAG GATCGNTTGA ACCTAGGGAG     540
GGAGGAGTTG GAGTGAGCTA ATGTCAATGC ACTCTTGGTT GGGGCGANAG AGCAAGATCT     600
TTCTTCCAAA AAAAAAAAAA AAAAAAAGC CAGGTGNGGN GGTCAAGGCT GTAATCCAGA     660
ATTNGGGAGG CCGNGGAGGN NATCANTGNG GNAGGNGTCA AGNGGGGCNG GCCACATGGG     720
GAACCCGTTN TTNTTAAATN AAAATTAGCC GGGGNGGGGG AGGACTNTAT CCNGTTCCGG     780
NGGTGNGGAG GATCNTTATT NTGGNGGAGG GTGGATGNNC CAGTTGACNC CCCC          834
```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
TTGGGCNCNC GCCCCTTAAN TTTTATNGN TTNCTANAAA AANANNNGGC NCNNTAAAT      60
ATATTTTTTN TTGTGACCCC TTTTAAAGG GACCCNCTAA AAAATTTTNT GGTTNNTTN      120
```

GATTTANGTG	GGTGNTTTTN	TTATATTTTT	GGNGAGNNTC	TGTAGTCNTC	NCCCTCAAAC	180
ANNTCNTACN	ATNGGNANCG	TGACTCTGTC	NTTNGTNANN	NTCGNTNTCN	NGTNATTENA	240
GGNNCCTCGC	GCNNCNCGGG	CNNNGTTTTT	TTTNNCNCNTT	TTTAAGCCNA	ANNCTCAGTA	300
NCNTCCAACG	GNGCTNNGAC	ANNNGNNNCT	NTCGNGGGTN	CCCTCTNTNT	NGNNCNGGGC	360
TNNNGNMMNC	NGNCNGCNGN	GCCNTGCGNN	NNGNNNGNGG	NNNGNTNNCA	TANGGATNGN	420
GNTGCTCNC	NCNNGNGTNN	TNAGTAGGNA	NTTTTNTNTT	ACTTGCCNNC	NNNTNGCTGC	480
GAGNANAGCN	ANNTNGNNGN	AGNGNNGNTG	CGCGGANNTT	CCCCTGATNA	NCTCGAGCNG	540
NTTACNGGNG	CNNCCTNGAA	NAAGNGNNGT	ANNGTGCCGA	GNCGCTANNC	TGAGCCTGAG	600
TNTCGACNGG	NATNGTGNN	CNTACNGTTA	NGGGNNGCNN	GANCGGGNTG	ANTCNCCGGN	660
NGANCNAGCG	ACTGCCTNTC	ANGCGAANCG	TNTCANGNNN	GTAGAGCANA	GGGTNANNNG	720
TCNNMNAAGC	NTNAGTGAN	TGTCNTNACN	NGTGANTTAC	GGCNTAGNCT	TGATNTNNAN	780
NCGAGGNMNN	ATNNANNNTT	GGANANTTNN	TNNNNTCNCN	TCGCGGNGNG	NCNNGCCG	838

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATTCGCGCGT	AGCCCATAA	CTATAGGGCG	ACNTGGAGNT	CCACCGCGGT	GGCGGCCGCT	60
CTAGNAACTA	GTGGATCCCC	CGGGCTGCAG	GAATTCACGG	ACTAATCCTC	TACAGATCTT	120
GCTGGAGTGG	CCTTTCAGCC	TTTTGTGACT	GTTTGTAGTG	AAATGTACAC	ACAAGCCTAC	180
AAGGCAGCCC	AGATGTACCA	TAACTGTGGG	AAAATTAAAA	AAAAAAAAAC	ACAGAACCTC	240
TCTATGTTGC	CCATGCTGGA	CTCAAACCTC	TAGACAAGCA	ATCCTCGTAC	CTCAGCCTCC	300
TGAGTTCCTG	AGTAGCTGGG	ACTACAAGCA	TGCACCACCA	TGCCAGGCTA	TGAGAAAGTT	360
CTTTTTATTG	ATCCAGACCT	TATTGCCTGG	TAACTTCCAC	CACGTGTCCT	AGCTCTGNTC	420
TCTGGTCCTA	ACAGAGGAAA	ATCTTGACCC	CACACCTAGT	GCAACTGGAT	AGCTTATNGT	480
TGGGCTNGTG	TTTCCTCTAT	TCTGGGTCCA	CCCTAAAATC	CNATAGATAC	TCCAACCTGT	540
CANAGNAAAC	CAAGCTCTCT	CTCTNNCTTN	CTTTCTTNNN	CTCTATTNAT	TNATGGGNNA	600

TNATTNATTN NGGGGATGGN GTTCGGTCGC CGCCCGGCTG GNGTGAAATG GGGGAGGCAA	660
TCAATTTAAC CCCACCCNGG GTCCAGGGAT CTCGTTNAAA CCGNNNNNNN NNNNNNNNNA	720
NGNNCNNCNC NNNCCNNTNN NNNGGTTTNN NNGNNNNNGG NNNCCNNNNN NANNNNNNTN	780
NNNCCNCCNA NNNTNCNNNN CCC	803

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CNNNNNNNCC CNNTNATTNT ACGCCAGCCG CGTAATTAAC CCTCACTAAA GGGAACAAAA	60
GCTGGGTACC GGGCCCCCCC TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCA	120
ACTCCTCACT TGCCAGATGT GACCTTAAGC AAGTGAAC TT CTGTGTGCCA CACTGTTTTTC	180
ATCTGTAAAA GGATAAAGGG AATATCATAA ATTAGNTTGT TAAGCCTTAG TTTAATAATG	240
TCTCTAAGTT TTACATATAA GTAGACAGTG TCTTTCTTGT TTAGTGAATA ATCATTCTTA	300
TTATTTAATA GTATCTCTAC TAAATTTATT GTGTAAGATT ATACTAATCT TGTTTAGTGC	360
GTGGTAATCA CTTCTGCTCA TATTTAACCT ATAAGCATAA TATAGTTTAT TTATATACCA	420
NTTATTTATT TTATTTTATT TGNNGAGATG CAGCTTGTCT TTTNCAACCC AGGGNTGNGG	480
NGNAGNNGNG NAANCTTGNT TCACTGNAAC CNCCACCNC CAGGTNCAAG NGATTCTCCT	540
GNTCAAGCCN CCTNAGNAGN TGGNATTACA GNACGANTAC ANNCCAGNTA NNNNGGNTNT	600
NNGNTNGNNA GGNNNCACAN NNGNCAGGTN NNTCGNCTCC NNGCCANTNA CTNNNNCCAN	660
CCCCNNNGNN NNNNATANAG NATNANCANN NNCCNCNNNN NCNNNNNNNG GNGGANNCCN	720
NNTNGCNGNN ANNGNNANNN NNTNNNNNNN NNGGNCNNNG NNNNNNNNCC NNNNNNCCCC	780

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

NNNNNNNNNC	CNNNNNNNTTC	GNNCGTAACN	CGANTCACTA	TAGGGCGACT	TGGAGCTCCA	60
CCGCGGTGGC	GGCCGCTCTA	GAAGTAGTGG	ATCCCCCGGG	CTGCAGGAAT	TCGATATCAA	120
GCTTTNGTGT	GTAAAAAGTA	TTAGAATCTC	ATGTTTTTTGA	ACAAGGTTGG	CAGTGGGTTG	180
GGAGGAGGGA	TTGGAGATTG	ATGCGATAGG	AATGTGAAGG	GATAGCTTGG	GGTGGATTTT	240
ATTTTTTAAT	TTTAATTTTT	ATTTNTTGAG	ATGGAGTCTT	GCTCTGTCTC	CCAGGCTGGA	300
GTGCAGTGGT	GTGATCTCAG	CTCACGGGTT	CAAGCGATTC	TCCTGCTGCA	GCCTCCCGAG	360
TAGCTGGGAT	TACAGGAGCG	CGCCACCACA	CCCGGNTAAT	TTNNTTGTAT	TTTTAGTAGA	420
GACGGGGTTT	CACCATGTTG	GTTAGGCTGG	TCTAGAACTC	CCAACCTCAT	GATCCGCCTG	480
CTTCGGCCTC	CCAAAGTGCC	GGAATTACAG	GCGTGAGCGA	CTGCACCCGG	CCGCTTGGGG	540
GTGGATTTTT	AAAGAAATTT	AGAAGAATGT	AACTTGGCCA	GATACCATGT	ACCCGTTAAT	600
TCATTTNCGG	TTTTTTGGAT	ACCCATTTTG	NNATTCTCCC	NCCACTGGAT	AAATAAGGGN	660
GGTTCATTNT	NGNTTAGTTT	GGGTNTTTTT	NAGTGTGGNT	TCTGCTTATN	ATTAGAATGG	720
NCTNCTTTNC	CAANCTGGAA	AGGGAGGAGT	TAAAATCANT	ACCAGAAACA	GAAATTCTTT	780
TCANTTGTTG	CNCNAGAAAT	GCC				803

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TNCCNNNNCN	NNNNNAATTT	TNGCAGNCGC	GTAATTAACC	TCACTAAAGG	GAACAAAAGC	60
TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTCCCTCC	CCTTCCTCAG	120
CTCTGGCGAC	CCTGCGCTGT	GGTGGTTCTC	CAACCACACT	CATTCTCCTC	AGCTGGCTCC	180
TTGCTCTTCT	TCCACCCCTT	CGTTGGAAGT	GTTCCTAAGT	GTTTGGCTTG	GCCTCCTCTT	240
CCCCTTCCTT	AGNTTAGACT	TCTCCACTGC	TCCAACATCA	ACTGGAAATC	TATGGAATTG	300
ATTCCTGTTT	TCAGCTCCAG	TCCTGTTTAC	AGGGCATTTC	CACCTGCTGG	CACTTCCAAA	360
GTGACACTTC	CAAACCACTT	CCTCGCCCTC	CTCTCTAAAC	CAGGTCTTTC	TTCCTAACTT	420
CCTTATTCTT	GAGAATGTCT	CTGNCATGTT	CTAAACTGAA	AACTCCTAGT	CAACTNCACA	480

CTTTATTCCC TGGATCCTCA ATTGGGTTCC CATGTNCCGT TAGTGTTTCT TGGTAAGNCT	540
CTGCCANCAC CGNAGGATCG ACTCTAATCA CATCTCAACT GAATTATGGN AAAGTCAACT	600
CAATTCTCTC AACCATCCCA GGCTCCACTA TGGNTAATAT GCTAAGGAGA GCTGACCCAA	660
CGGGGAGAAAG ATCTGNNGGG GAGGAGAGAA ACAAAGNTAA TGGAAATNATT CTCGAAAAGC	720
CCACAAGGNG AAGGATAACC CNCTTCCNCT CGAAAGAGGG GGGATCGCCA GATNTCGCGC	780
CCGGAAAGAA ACCGGGGNGA GGGGGTTACA NTGTAAGNC	819

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TNTTGGCTGG TACTGCTTGA GCAACTGGTG AAAC TCCGCG CCTCACGCCC CGGGTGTGTC	60
CTTGTCCAGG GCGGACGAGC ATTCTGGGCG AAGTCCGCAC GCCTCTTGTT CGAGGCGGAA	120
GACGGGGTCT GATGCTTTCT CCTTGGTCGG GACTGTCTCG AGGCATGCAT GTCCAGTGAC	180
TCTTGTGTTT GCTGCTGCTT CCCTCTCAGA TTCTTCTCAC CGTTGTGGTC AGCTCTGCTT	240
TAGGCATATT AATCCATAGT GGAGGCTGGG ATGGGTGAGA GAATTGAGGT GACTTTTCCA	300
TAATTCAGGT GAGATGTGAT TAGAGTTCGA TCTGCGGTGG TGGCAGAGGC TTACAAGAAA	360
CACTAACGGG ACATGGGAAC CAATTGAGGA TCAGGGAATA AAGTGTGAAG TTGACTAGGA	420
GGTTTTCACT TTAGAACATG GCAGAGACAT TCTCAGAAAT AAGGAAGTTA GGAAGAAAGA	480
CTGGTTTAGA GAGGAGGGCG ANGAAGTGGT TTGGGAAGTG TCACTTTGGG AAGTGCCAGC	540
AGGTGAAAAT GCCTGTGACA GGATGGAGCT GAAAACAGGA TCAATTCCAT AGATTCCAGT	600
TGATGTNGGA GCAGGGGAGA AGTCTTAGCT AAGGAAGGGG AAGAGGAGGC CAAGGNAACA	660
CTTAGGACAA TTGNAACGAN GGGGGGGGAG AAGAGNAAGG GCCACTTAGG GGAATAATNT	720
GGTGGGGGAC CCCCAGNNA GGGCGCANNN TTAGGAGGGG GGGANNTCAN AGGAAAGTGG	780
AAGNTTGGGT TTANCT	796

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 802 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTCGTCGTA NCCCGATNAC TATAGGGCGA CTTGGAGCTC CACCGCGGTG GCGGNCGCGG	60
GCAGGGNCCG GNCCTTTGTG GCCGCCCCGGG CCGCGAAGCC GGTGTCCTAA AAGATGAGGG	120
GCGGGGCGCG GNCGGTTGGG GCTGGGGAAC CCCGTGTGGG AAACCAGGAG GGGCGGCCCC	180
TTTCTCGGGC TTCGGGCGCG GCCGGGTGGA GAGAGATTCC GGGGAGCCTT GGTCCGAAA	240
TGCTGTTTGC TCGAAGACGT CTCAGGGCGC AGGTGCCTTG GGCCGGGATT AGTAGCCGTC	300
TGAACTGGAG TGGAGTAGGA GAAAGAGGAA GCGTCTTGGG CTGGGTCTGC TTGAGCAACT	360
GGTGAAACTC CGCGCCTCAC GCCCCGGGTG TGTCTTGTC CAGGGGCGAC GAGCATTCTG	420
GGCGAAGTCC GCACGCCTCT TGTTCGAGGC GGAAGACGGG GTCTTGATGC TTTCTCCTTG	480
GGTCGGGGAC TGTCTCGAGG CATGCATGTC CAGTGACTCT TGTGTTTGGT GNTGCTTCCC	540
TCTCAGATCT TCTCACCGNG GTGGGCAACT CTGTTTAGGC ATATTATCCA TAGNGGAGGC	600
TGGATGGTTG AAANAATTGA GGTNATTTTC CATAATCAAG TGAAATTTGA TAGAGTCCGN	660
CTTTNGGGGT GNAAGGGTTA AAAAAAATA ACGGAAATGG AACAATGAGG TCAAGGATTA	720
GTTGAGTTGN TAGNGGTTCA ATTAGANATG AAGGNATCTA AAATAGGAGT AGAGAANNNG	780
TTNAAAGAGG GAAAATTTTG CC	802

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 793 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATATGCAGCC GCGTAATTAA CCTCACTAAA GGGAACAAAA GCTGGGTACC GGGCCCCCCC	60
TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCT GCAGCCCGGG GGATCCGCCC	120
CGCGGCCTCC CAAAGTGCTG GGATTACAGG CGTGAGCCAC CGCCCCGGGN CTCACATTTT	180
ATTTCTATTG GCTAGCGCTG CTCTAAATCT TCTGTTTCCTT CTGCTACACC AGGCCTAACA	240

CTCAAAATCC CTGCCAACCT TTTCCTTCCT GAAGCTTGCC TCCCCTTCCT CAGCTCTGGC	300
GACCCTGCGC TGTGGTGGTT CTCCAACCAC ACTCATTCTC CTCAGCTGGC TCCTTGCTCT	360
TCTTCCACCC CCTCGNTGGA AGTGTTCCTA AGTGTTTGGC TTGGCCTCCT CTTCCCCTTC	420
CTTAGCTTAG ACTTCTCCAC TGCTCCAACA TCAACTGGAA ATCTATGGAA TTGATTCTGT	480
TTTCAGCTCC AGTCCTGTTT ACAGGGGATT TTCANCTGGT GGCATTTCCA AAGTGAAATT	540
CCAAACCACT TCCTCGGCCT CCTCTTCTAA ANCAGGTCTT TCTTCCTAAC TTCCTTATTC	600
TTGAGAATGT CTCTGCATGT TCTTAAANTG AAAACTCCTA GTCAAATTCA AATTTATCCC	660
TGATCCCAAA TGGTCCCATT CCCGTAGGGT TTNTGTAGCC TGCACACCGA GGTCGGANTT	720
TATNNATTCA CCGATTATGG AAAGTAACCA ATCTTNACCA NCCAGCTCAT TTGTTNTNTG	780
CTAAGAGGGT NCC	793

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAGTCATGG ATTCCTTTAG GTAGCTACAT TATCAACCTT TTTGAGAATA AAATGAATTG	60
AGAGTGTTAC AGTCTAATTC TATATCACAT GTAACTTTTA TTTGGATATA TCAGTAATAG	120
TGCTTTTTTCN TTTTTTTTTT TTNTTTTTTT TNNTTTTNGG GGANAGAGTC TCGCTCTGTC	180
GCCAGGTTGG AGTGCAATGG TGCGATCTTG GCTCACTGAA AGCTCCACCN CCCGGGTTC	240
AGTGATTCTC CTGCCTCAGC CNCCCAAGTA GNTGGGACTA CAGGGGTGCG CCACCACGCC	300
TGGGATAATT TTGGGNTTTT TAGTAGAGAT GGC GTTTCAC CANCTTGGNG CAGGCTGGTC	360
TTGGAACCTC TGANATCATG ATCTGCCTGC CTTAGCCTCC CCAAAGTGCT GGGATTNCAG	420
GGGTGAGCCA CTGTTCTCTGG	440

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTTAGTCTGT NTCGTAGTCA TATTAATTGT AAGTNTACAC TAATAAGAAT GTGTCAGAGC	60
TCTTAATGTC AAAACTTTGA TTACACAGTC CCTTTAAGGC AGTTCTGTTT TAACCCCAGG	120
TGGGTAAAT ATTCCAGCTA TCTGAGGAGC TTTTNGATAA TTGGACCTCA CCTTAGTAGT	180
TCTCTACCCT GGCCACACAT TAGAATCACT TGGGAGCTTT TAAAACTGTA AGCTCTGCCC	240
TGAGATATTC TTA CTCAATT TAATTGTGTA GTTTTTAAAA TTCCCAGGA AATTCTGGTA	300
TTTCTGTTTA GGAACCGCTG CCTCAAGCCT AGCAGNACAG ATATGTAGGA AATTAGCTCT	360
GTAAGGTTGG TCTTACAGGG GATAAACAGA TCCTTCCTTA GNCCCTGGGA CTTAATCACT	420
GAGAGTTTGG GTGGNGGTTT NGNATTTAAT GAC	453

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GACACACATT CACACATAAT TATGAAAGCA TTTTCAGGCA AACTCAATC ACAAGTCTGG	60
GTTTTTAACA TAGTAACTG AATATTTCCC TTGGGGGGTT AAATTTTAGA ACAGACGTNC	120
ATNCAATCTG GAAGAAGAGC TATGAAAAAA ACCTAGCTTG GGTNGGTTTC ATAGGGTNCA	180
TTATGNACAC ATTGTTATTT TATCCCTTAA TNCTAGTAAA GAAATAGAAT CTGAAAATAA	240
GTAAACTAC TTGGAAAAAA NTTAAAAGAT ACAGAAATTT CTATCTTAAA TGATGTGTGG	300
GCCNCTGTGA TTTTAGTNGG GNTGGTTAAA ANCCAGAGG TGAAGAGNAT NCTCTATGCT	360
GTGNGGGGG	369

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTCATCATG	CTTCACGGGG	GAGGCTGTGC	GGGAAGAATG	CTCCACACA	GNATAAGAA	60
TGCTCCCGCA	CAGGATAGAG	AATGCCCCCG	CACAGCATAG	AGAAGCCCCC	GCACAGCATA	120
GAGAA TGCCC	CCNCACAGCA	TAGAGAAGCC	CCCGCACAGC	ATAGAGAATG	CTCTTCACCT	180
CTGGGTTTTT	AACCAGCCAA	ACTAAAATCA	CAGAGGSCMA	CACATCATTT	AAGATAGAAA	240
TTTCTGTATC	TTTAAATTTY	TTTCMAAGTA	GTTTTACTTA	TTTTCAGATT	CTATTTCTTT	300
ACTAGAATTA	AGGGATAAAA	TAACAATGTG	TGCATAATGA	ACCCTATGAA	ACMAACMMAA	360
GCTAGGTTTT	TTTCATAGST	CTTCTTCCAG	ATTGAATGAA	CGTCTGTTCT	AAAATTTAAC	420
CCCCCAGGGA	AATATTCAGT	TAACATATGT	AAAAACCCAG	ACTTGTGATT	GAGTTTTGCC	480
TGAAAATGCT	TTCATAATTA	TGTGTGAATG	TGTGTC			516

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTATAATGCA	GGTGCTATAA	GGTGAGCATG	AGACACAGAT	CTTTGCTTTC	CACCCTGTTC	60
TTCTTATGGT	TGGGTATTCT	TGTCACAGTA	ACTTAACTGA	TCTAGGAAAG	AAAAAATGTT	120
T						121

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TGGAGACTGG AACACAAC

18

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGTGGCCAG GGTAGAGAAC T

21

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATCTCCGGCA GGCATATCT

19

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGAAATCACA GCCAAGATGA G

21

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CCATAGCCTG TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CCATAGCCTA TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2791 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCAAT GACAGAGTTA CCTGCACCGT TGTCCTACTT CCAGAATGCA CAGATGTCTG	300
AGGACAACCA CCTGAGCAAT ACTGTACGTA GCCAGAATGA CAATAGAGAA CGGCAGGAGC	360
ACAACGACAG ACGGAGCCTT GGCCACCCTG AGCCATTATC TAATGGACGA CCCCAGGGTA	420
ACTCCCGGCA GGTGGTGGAG CAAGATGAGG AAGAAGATGA GGAGCTGACA TTGAAATATG	480

GCGCCAAGCA	TGTGATCATG	CTCTTTGTCC	CTGTGACTCT	CTGCATGGTG	GTGGTCGTGG	540
CTACCATTAA	GTCAGTCAGC	TTTTATACCC	GGAAGGATGG	GCAGCTAATC	TATACCCCAT	600
TCACAGAAGA	TACCGAGACT	GTGGGCCAGA	GAGCCCTGCA	CTCAATTCTG	AATGCTGCCA	660
TCATGATCAG	TGTCATTGTT	GTCATGACTA	TCCTCCTGGT	GGTTCCTGTAT	AAATACAGGT	720
GCTATAAGGT	CATCCATGCC	TGGCTTATTA	TATCATCTCT	ATTGTTGCTG	TTCTTTTTTT	780
CATTCAATTA	CTTGGGGGAA	GTGTTTAAAA	CCTATAACGT	TGCTGTGGAC	TACATTACTG	840
TTGCACTCCT	GATCTGGAAT	TTTGGTGTGG	TGGGAATGAT	TTCCATTAC	TGGAAAGGTC	900
CACTTCGACT	CCAGCAGGCA	TATCTCATTA	TGATTAGTGC	CCTCATGGCC	CTGGTGTTTA	960
TCAAGTACCT	CCCTGAATGG	ACTGCGTGGC	TCATCTTGGC	TGTGATTTC	GTATATGATT	1020
TAGTGGCTGT	TTTGTGTCCG	AAAGGTCCAC	TTCGTATGCT	GGTTGAAACA	GCTCAGGAGA	1080
GAAATGAAAC	GCTTTTTCCA	GCTCTCATTT	ACTCCTCAAC	AATGGTGTGG	TTGGTGAATA	1140
TGGCAGAAGG	AGACCCGGAA	GCTCAAAGGA	GAGTATCCAA	AAATTCCAAG	TATAATGCAG	1200
AAAGCACAGA	AAGGGAGTCA	CAAGACACTG	TTGCAGAGAA	TGATGATGGC	GGGTTCAGTG	1260
AGGAATGGGA	AGCCCAGAGG	GACAGTCATC	TAGGGCCTCA	TCGCTCTACA	CCTGAGTCAC	1320
GAGCTGCTGT	CCAGGAACTT	TCCAGCAGTA	TCCTCGCTGG	TGAAGACCCA	GAGGAAAGGG	1380
GAGTAAAACT	TGGATTGGGA	GATTTCAATTT	TCTACAGTGT	TCTGGTTGGT	AAAGCCTCAG	1440
CAACAGCCAG	TGGAGACTGG	AACACAACCA	TAGCCTGTTT	CGTAGCCATA	TTAATTGGTT	1500
TGTGCCTTAC	ATTATTACTC	CTTGCCATTT	TCAAGAAAGC	ATTGCCAGCT	CTTCCAATCT	1560
CCATCACCTT	TGGGCTTGTT	TTCTACTTTG	CCACAGATTA	TCTTGACAG	CCTTTTATGG	1620
ACCAATTAGC	ATTCCATCAA	TTTTATATCT	AGCATATTTG	CGGTTAGAAT	CCCATGGATG	1680
TTTCTTCTTT	GACTATAACC	AAATCTGGGG	AGGACAAAGG	TGATTTTCCT	GTGTCCACAT	1740
CTAACAAAGT	CAAGATTCCC	GGCTGGACTT	TTGCAGCTTC	CTTCCAAGTC	TTCCTGACCA	1800
CCTTGCACTA	TTGGACTTTG	GAAGGAGGTG	CCTATAGAAA	ACGATTTTGA	ACATACTTCA	1860
TCGCAGTGGA	CTGTGTCCCT	CGGTGCAGAA	ACTACCAGAT	TTGAGGGACG	AGGTCAAGGA	1920
GATATGATAG	GCCCCGGAAGT	TGCTGTGCCC	CATCAGCAGC	TTGACGCGTG	GTCACAGGAC	1980
GATTTCACTG	ACACTGCGAA	CTCTCAGGAC	TACCGGTTAC	CAAGAGGTTA	GGTGAAGTGG	2040
TTTAAACCAA	ACGGAACCTCT	TCATCTTAAA	CTACACGTTG	AAAATCAACC	CAATAATTCT	2100
GTATTAAGTG	AATTCTGAAC	TTTTCAGGAG	GTAAGTGTGAG	GAAGAGCAGG	CACCAGCAGC	2160
AGAATGGGGA	ATGGAGAGGT	GGGCAGGGGT	TCCAGCTTCC	CTTTGATTTT	TTGCTGCAGA	2220


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CTCATCCTTT TTAAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA      2280
TTGCCTTTGG CAATTCTTCT TCTCAAGCAC TGACACTCAT TACCGTCTGT GATTGCCATT      2340
TCTTCCAAG GCCAGTCTGA ACCTGAGGTT GCTTTATCCT AAAAGTTTTA ACCTCAGGTT      2400
CCAAATTCAG TAAATTTTGG AAACAGTACA GCTATTTCTC ATCAATTCTC TATCATGTTG      2460
AAGTCAAATT TGGATTTTCC ACCAAATTCT GAATTTGTAG ACATACTTGT ACGCTCACTT      2520
GCCCCCAGAT GCCTCCTCTG TCCTCATTCT TCTCTCCAC ACAAGCAGTC TTTTCTACA      2580
GCCAGTAAGG CAGCTCTGTC TGGTAGCAGA TGGTCCCATT ATTCTAGGGT CTTACTCTTT      2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC      2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG      2760
AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A                                     2791

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(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1              5              10              15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20              25              30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35              40              45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50              55              60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65              70              75              80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85              90              95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100            105            110

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Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg		
		115					120					125					
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val		
	130					135					140						
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys		
145				150						155					160		
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe		
				165					170					175			
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala		
			180					185					190				
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val		
	195						200					205					
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala		
	210					215					220						
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr		
225				230					235						240		
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr		
				245					250					255			
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val		
		260						265					270				
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr		
		275					280					285					
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu		
	290					295					300						
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	Tyr	Asn	Ala	Glu	Ser	Thr		
305				310						315					320		
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe		
				325					330					335			
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg		
			340					345					350				
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile		
		355					360					365					
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly		
	370					375					380						
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala		
385					390					395					400		
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile		
				405					410					415			

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 450 455 460

Phe Tyr Ile
 465

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCANACANC GGCAGCTGAG GCGGAAACCT AGGCTGCGAG CCGGCCGCCC GGGCGCGGAG	60
AGAGAAGGAA CCAACACAAG ACAGCAGCCC TTCGAGGTCT TTAGGCAGCT TGGAGGAGAA	120
CACATGAGAG AAAGAATCCC AAGAGGTTTT GTTTTCTTTG AGAAGGTATT TCTGTCCAGC	180
TGCTCCAATG ACAGAGATAC CTGCACCTTT GTCCTACTTC CAGAATGCCC AGATGTCTGA	240
GGACAGCCAC TCCAGCAGCG CCATCCGGAG CCAGAATGAC AGCCAAGAAC GGCAGCAGCA	300
GCATGACAGG CAGAGACTTG ACAACCCTGA GCCAATATCT AATGGGCGGC CCCAGAGTAA	360
CTCAAGACAG GTGGTGGAA CAGATGAGGA GGAAGACGAA GAGCTGACAT TGAAATATGG	420
AGCCAAGCAT GTCATCATGC TCTTTGTCCC CGTGACCCTC TGCATGGTCG TCGTCGTGGC	480
CACCATCAAA TCAGTCAGCT TCTATACCCG GAAGGACGGT CAGCTAATCT ACACCCCATT	540
CACAGAAGAC ACTGAGACTG TAGGCCAAAG AGCCCTGCAC TCGATCCTGA ATGCGGCCAT	600
CATGATCAGT GTCATTGTCA TTATGACCAT CCTCCTGGTG GTCCTGTATA AATACAGGTG	660
CTACAAGGTC ATCCACGCCT GGCTTATTAT TTCATCTCTG TTGTTGCTGT TCTTTTTTTC	720
GTTCAATTTAC TTAGGGGAAG TATTTAAGAC CTACAATGTC GCCGTGGACT ACGTTACAGT	780
AGCACTCCTA ATCTGGAATT TTGGTGTGGT CGGGATGATT GCCATCCACT GGAAAGGCCC	840
CCTTCGACTG CAGCAGGCGT ATCTCATTAT GATCAGTGCC CTCATGGCCC TGGTATTTAT	900

CAAGTACCTC	CCCGAATGGA	CCGCATGGCT	CATCTTGGCT	GTGATTTCAG	TATATGATTT	960
GGTGGCTGTT	TTATGTCCCA	AAGGCCCACT	TCGTATGCTG	GTTGAAACAG	CTCAGGAAAG	1020
AAATGAGACT	CTCTTTCCAG	CTCTTATCTA	TTCCTCAACA	ATGGTGTGGT	TGGTGAATAT	1080
GGCTGAAGGA	GACCCAGAAG	CCCAAAGGAG	GGTACCCAAG	AACCCCAAGT	ATAACACACA	1140
AAGAGCGGAG	AGAGAGACAC	AGGACAGTGG	TTCTGGGAAC	GATGATGGTG	GCTTCAGTGA	1200
GGAGTGGGAG	GCCCCAAGAG	ACAGTCACCT	GGGGCCTCAT	CGCTCCACTC	CCGAGTCAAG	1260
AGCTGCTGTC	CAGGAACTTT	CTGGGAGCAT	TCTAACGAGT	GAAGACCCGG	AGGAAAGAGG	1320
AGTAAACTT	GGACTGGGAG	ATTTTCATTTT	CTACAGTGTT	CTGGTTGGTA	AGGCCTCAGC	1380
AACCGCCAGT	GGAGACTGGA	ACACAACCAT	AGCCTGCTTT	GTAGCCATAC	TGATCGGCCT	1440
GTGCCTTACA	TTACTCCTGC	TCGCCATTTT	CAAGAAAGCG	TTGCCAGCCC	TCCCCATCTC	1500
CATCACCTTC	GGGCTCGTGT	TCTACTTCGC	CACGGATTAC	CTTGTGCAGC	CCTTCATGGA	1560
CCAACTTGCA	TTCCATCAGT	TTTATATCTA	GCCTTTCTGC	AGTTAGAACA	TGGATGTTTC	1620
TTCTTTGATT	ATCAAAAACA	CAAAAACAGA	GAGCAAGCCC	GAGGAGGAGA	CTGGTGACTT	1680
TCCTGTGTCC	TCAGCTAACA	AAGGCAGGAC	TCCAGCTGGA	CTTCTGCAGC	TTCCTTCCGA	1740
GTCTCCCTAG	CCACCCGCAC	TACTGGACTG	TGGAAGGAAG	CGTCTACAGA	GGAACGGTTT	1800
CCAACATCCA	TCGCTGCAGC	AGACGGTGTC	CCTCAGTGAC	TTGAGAGACA	AGGACAAGGA	1860
AATGTGCTGG	GCCAAGGAGC	TGCCGTGCTC	TGCTAGCTTT	GACCGTGGGC	ATGGAGATTT	1920
ACCCGCACTG	TGAACTCTCT	AAGGTAAACA	AAGTGAGGTG	AACC		1964

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCA	CGAGGGCATT	TCCAGCAGTG	AGGAGACAGC	CAGAAGCAAG	CTTTTGGAGC	60
TGAAGGAACC	TGAGACAGAA	GCTAGTCCCC	CCTCTGAATT	TTACTGATGA	AGAACTGAG	120
GCCACAGAGC	TAAAGTGACT	TTTCCCAAGG	TCGCCAGCG	AGGACGTGGG	ACTTCTCAGA	180

CGTCAGGAGA	GTGATGTGAG	GGAGCTGTGT	GACCATAGAA	AGTGACGTGT	TAAAAACCAG	240
CGCTGCCCTC	TTTGAAAGCC	AGGGAGCATC	ATTCATTTAG	CCTGCTGAGA	AGAAGAAACC	300
AAGTGTCGG	GATTCAAGAC	CTCTCTGCGG	CCCCAAGTGT	TCGTGGTGCT	TCCAGAGGCA	360
GGGCTATGCT	CACATTTCATG	GCCTCTGACA	GCGAGGAAGA	AGTGTGTGAT	GAGCGGACGT	420
CCCTAATGTC	GGCCGAGAGC	CCCACGCCGC	GCTCCTGCCA	GGAGGGCAGG	CAGGGCCCAG	480
AGGATGGAGA	GAATACTGCC	CAGTGGAGAA	GCCAGGAGAA	CGAGGAGGAC	GGTGAGGAGG	540
ACCCTGACCG	CTATGTCTGT	AGTGGGGTTC	CCGGGCGGCC	GCCAGGCCTG	GAGGAAGAGC	600
TGACCCTCAA	ATACGGAGCG	AAGCATGTGA	TCATGCTGTT	TGTGCCTGTC	ACTCTGTGCA	660
TGATCGTGGT	GGTAGCCACC	ATCAAGTCTG	TGCGCTTCTA	CACAGAGAAG	AATGGACAGC	720
TCATCTACAC	GCCATTCACT	GAGGACACAC	CCTCGGTGGG	CCAGCGCCTC	CTCAACTCCG	780
TGCTGAACAC	CCTCATCATG	ATCAGCGTCA	TCGTGGTTAT	GACCATCTTC	TTGGTGGTGC	840
TCTACAAGTA	CCGCTGCTAC	AAGTTCATCC	ATGGCTGGTT	GATCATGTCT	TCACTGATGC	900
TGCTGTTTCT	CTTCACCTAT	ATCTACCTTG	GGGAAGTGCT	CAAGACCTAC	AATGTGGCCA	960
TGGACTACCC	CACCCTCTTG	CTGACTGTCT	GGAAC TTCGG	GGCAGTGGGC	ATGGTGTGCA	1020
TCCACTGGAA	GGGCCCTCTG	GTGCTGCAGC	AGGCCTACCT	CATCATGATC	AGTGCCTCA	1080
TGGCCCTAGT	GTTTCATCAAG	TACCTCCCAG	AGTGGTCCGC	GTGGGTCATC	CTGGGCGCCA	1140
TCTCTGTGTA	TGATCTCGTG	GCTGTGCTGT	GTCCCAAAGG	GCCTCTGAGA	ATGCTGGTAG	1200
AAACTGCCCA	GGAGAGAAAT	GAGCCCATAT	TCCCTGCCCT	GATATACTCA	TCTGCCATGG	1260
TGTGGACGGT	TGGCATGGCG	AAGCTGGACC	CCTCCTCTCA	GGGTGCCCTC	CAGCTCCCCT	1320
ACGACCCGGA	GATGGAAGAA	GACTCCTATG	ACAGTTTTTG	GGAGCCTTCA	TACCCCGAAG	1380
TCTTTGAGCC	TCCCTTGACT	GGCTACCCAG	GGGAGGAGCT	GGAGGAAGAG	GAGGAAAGGG	1440
GCGTGAAGCT	TGGCCTCGGG	GACTTCATCT	TCTACAGTGT	GCTGGTGGGC	AAGGCGGCTG	1500
CCACGGGCAG	CGGGGACTGG	AATACCACGC	TGGCCTGCTT	CGTGGCCATC	CTCATTGGCT	1560
TGTGTCTGAC	CCTCCTGCTG	CTTGCTGTGT	TCAAGAAGGC	GCTGCCCCGCC	CTCCCCATCT	1620
CCATCACGTT	CGGGCTCATC	TTTTACTTCT	CCACGGACAA	CCTGGTGCGG	CCGTTTCATGG	1680
ACACCCTGGC	CTCCCATCAG	CTCTACATCT	GAGGGACATG	GTGTGCCACA	GGCTGCAAGC	1740
TGCAGGGAAT	TTTCATTGGA	TGCAGTTGTA	TAGTTTTTACA	CTCTAGTGCC	ATATATTTTT	1800
AAGACTTTTC	TTTCCTTAAA	AAATAAAGTA	CGTGTTTTACT	TGGTGAGGAG	GAGGCAGAAC	1860
CAGCTCTTTG	GTGCCAGCTG	TTTCATCACC	AGACTTTGGC	TCCCGCTTTG	GGGAGCGCCT	1920

CGCTTCACGG ACAGGAAGCA CAGCAGGTTT ATCCAGATGA ACTGAGAAGG TCAGATTAGG 1980
 GTGGGGAGAA GAGCATCCGG CATGAGGGCT GAGATGCCCA AAGAGTGTGC TCGGGAGTGG 2040
 CCCCTGGCAC CTGGGTGCTC TGGCTGGAGA GGAAAAGCCA GTTCCCTACG AGGAGTGTTT 2100
 CCAATGCTTT GTCCATGATG TCCTTGTTAT TTTATTNCCY TTANAACTG ANTCCTNTTN 2160
 TTNTTDCGGC AGTCACMCTN CTGGGRAGTG GCTTAATAGT AANATCAATA AANAGNTGAG 2220
 TCCTNTTAGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2280
 AAAAA 2285

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Met	Leu	Thr	Phe	Met	Ala	Ser	Asp	Ser	Glu	Glu	Glu	Val	Cys	Asp	Glu	1	5	10	15
Arg	Thr	Ser	Leu	Met	Ser	Ala	Glu	Ser	Pro	Thr	Pro	Arg	Ser	Cys	Gln	20	25	30	
Glu	Gly	Arg	Gln	Gly	Pro	Glu	Asp	Gly	Glu	Asn	Thr	Ala	Gln	Trp	Arg	35	40	45	
Ser	Gln	Glu	Asn	Glu	Glu	Asp	Gly	Glu	Glu	Asp	Pro	Asp	Arg	Tyr	Val	50	55	60	
Cys	Ser	Gly	Val	Pro	Gly	Arg	Pro	Pro	Gly	Leu	Glu	Glu	Glu	Leu	Thr	65	70	75	80
Leu	Lys	Tyr	Gly	Ala	Lys	His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	85	90	95	
Leu	Cys	Met	Ile	Val	Val	Val	Ala	Thr	Ile	Lys	Ser	Val	Arg	Phe	Tyr	100	105	110	
Thr	Glu	Lys	Asn	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	115	120	125	
Pro	Ser	Val	Gly	Gln	Arg	Leu	Leu	Asn	Ser	Val	Leu	Asn	Thr	Leu	Ile	130	135	140	
Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu	Val	Val	Leu	Tyr	145	150	155	160

Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu	Ile	Met	Ser	Ser	
				165					170					175		
Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu	Gly	Glu	Val	Leu	
				180				185					190			
Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu	Leu	Leu	Thr	Val	
		195					200					205				
Trp	Asn	Phe	Gly	Ala	Val	Gly	Met	Val	Cys	Ile	His	Trp	Lys	Gly	Pro	
	210					215					220					
Leu	Val	Leu	Gln	Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	
225					230					235					240	
Leu	Val	Phe	Ile	Lys	Tyr	Leu	Pro	Glu	Trp	Ser	Ala	Trp	Val	Ile	Leu	
				245					250					255		
Gly	Ala	Ile	Ser	Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	
			260					265					270			
Pro	Leu	Arg	Met	Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Pro	Ile	
		275					280					285				
Phe	Pro	Ala	Leu	Ile	Tyr	Ser	Ser	Ala	Met	Val	Trp	Thr	Val	Gly	Met	
	290					295					300					
Ala	Lys	Leu	Asp	Pro	Ser	Ser	Gln	Gly	Ala	Leu	Gln	Leu	Pro	Tyr	Asp	
305					310					315					320	
Pro	Glu	Met	Glu	Glu	Asp	Ser	Tyr	Asp	Ser	Phe	Gly	Glu	Pro	Ser	Tyr	
			325						330					335		
Pro	Glu	Val	Phe	Glu	Pro	Pro	Leu	Thr	Gly	Tyr	Pro	Gly	Glu	Glu	Leu	
			340					345					350			
Glu	Glu	Glu	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	Asp	Phe	Ile	
	355						360					365				
Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ala	Ala	Thr	Gly	Ser	Gly	Asp	
	370					375					380					
Trp	Asn	Thr	Thr	Leu	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	Gly	Leu	Cys	
385					390					395					400	
Leu	Thr	Leu	Leu	Leu	Leu	Ala	Val	Phe	Lys	Lys	Ala	Leu	Pro	Ala	Leu	
				405					410					415		
Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Ile	Phe	Tyr	Phe	Ser	Thr	Asp	Asn	
			420					425					430			
Leu	Val	Arg	Pro	Phe	Met	Asp	Thr	Leu	Ala	Ser	His	Gln	Leu	Tyr	Ile	
		435					440					445				

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	His	Val	Ile	Met	Leu	Phe	1	5	10	15
Val	Pro	Val	Thr	Leu	Cys	Met	Ile	Val	Val	Val	Ala	Thr	Ile	Lys	Ser	20	25	30	
Val	Arg	Phe	Tyr	Thr	Glu	Lys	Asn	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	35	40	45	
Thr	Glu	Asp	Thr	Pro	Ser	Val	Gly	Gln	Arg	Leu	Leu	Asn	Ser	Val	Leu	50	55	60	
Asn	Thr	Leu	Ile	Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu	65	70	75	80
Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu	85	90	95	
Ile	Met	Ser	Ser	Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu	100	105	110	
Gly	Glu	Val	Leu	Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu	115	120	125	
Leu	Leu	Thr	Val	Trp	Asn	Phe	Gly	Ala	Val	Gly	Met	Val	Cys	Ile	His	130	135	140	
Trp	Lys	Gly	Pro	Leu	Val	Leu	Gln	Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	145	150	155	160
Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr	Leu	Pro	Glu	Trp	Ser	Ala	165	170	175	
Trp	Val	Ile	Leu	Gly	Ala	Ile	Ser	Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	180	185	190	
Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	195	200	205	
Asn	Glu	Pro	Ile	Phe	Pro	Ala	Leu	Ile	Tyr	Ser	Ser	Ala	Met	Val	Trp	210	215	220	
Thr	Val	Gly	Met	Ala	Lys	Leu	Asp	Pro	Ser	Ser	Gln	Gly	Ala	Leu	Gln	225	230	235	240
Leu	Pro	Tyr	Asp	Pro	Glu	Met	Glu	Glu	Asp	Ser	Tyr	Asp	Ser	Phe	Gly	245	250	255	

Glu	Pro	Ser	Tyr	Pro	Glu	Val	Phe	Glu	Pro	Pro	Leu	Thr	Gly	Tyr	Pro
			260					265					270		
Gly	Glu	Glu	Leu	Glu	Glu	Glu	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu
		275					280					285			
Gly	Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ala	Ala	Thr
	290					295					300				
Gly	Ser	Gly	Asp	Trp	Asn	Thr	Thr	Leu	Ala	Cys	Phe	Val	Ala	Ile	Leu
305					310					315					320
Ile	Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Val	Phe	Lys	Lys	Ala
			325					330						335	
Leu	Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Ile	Phe	Tyr	Phe
		340						345					350		
Ser	Thr	Asp	Asn	Leu	Val	Arg	Pro	Phe	Met	Asp	Thr	Leu	Ala	Ser	His
		355					360					365			
Gln	Leu	Tyr	Ile												
	370														

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGTACCGCCA CCATGACAGA GGTACCTGCA C

31

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCACTG GCTGTAGAAA AAGAC

25

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCGGTC CACTTCGTAT GCTG

24

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTTTTTGAAT TCTTAGGCTA TGGTTGTGTT CCA

33

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATTAGTGGT TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:144:

164a

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATTAGTGGC TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTTTTCCAGC TCTCATTTA

19

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TTTTTCCAGT TCTCATTTA

19

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TACAGTGTTT TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TACAGTGTTT TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TACAGTGTTT TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCTAGATAA GNCAACATTC AGGGGTAGAA GGGGACTGTT TATTTTTTCC TTTAGTCTCT	60
CTTAAAGAGT GAGAAAAATT TTCCCAGGAA TCCCGGTGGA CTTTGCTTCA CCACTCATAG	120
GTTCATACCA AGTTACAACC CCACAACCTT AGAGCTTTTG TTAGGAAGAG GCTTGGTGGG	180
ATTACCGTGC TTGGCTTGGC TTGGTCAGGA TTCACCACCA GAGTCATGTG GGAGGGGGTG	240
GGAACCCAAA CAATTCAGGA TTCTGCCCTC AGGAAATAAA GGAGAAAATA GCTGTTGGAT	300
AAACTACCAG CAGGCACTGC TACAGCCCAT GCTTTGTGGT TTAAGGGCCA GCTAGTTACA	360
ATGACAGCTA GTTACTGTTT CCATGTAATT TTCTTAAAGG TATTAAATTT TTCTAAATAT	420
TAGAGCTGTA ACTTCCACTT TCTCTGAAG GCACAGWAAG GGAGTCACAA GAACTGTTG	480
CAGAGAATGA TGATGGCGGG TTCAGTGAGG AATGGGAASC CCAGRGGGAC ANTCATCTAG	540
GGCCTCATCG CTCTACACCT GAGTCACGAG CTKCTNTCCA GGRACCTTCC ANCAGTATCC	600
TCGCTGGTGA AGACCCAGAG GAAAGNATGT TCANTTCTCC ATNTTTCAAA GTCATGGATT	660
CCTTTAGGTA GCTACATTAT CAACCTTTTT GAGAATAAAA TGAATTGAGA GTGTTACAGT	720
CTAATTCTAT ATCACATGTA ACTTTTATTT GGATATATCA GTAATAGTGC TTTTNTTTT	780
TTTTTTTTTT TTTTTTTTTT TTTTNGGNGA NAGAGTCTCG CTCTGTCGCC AGGTTGGAGT	840
GCAATGGTGC GATCTTGGCT CACTGAAAGC TCCACCNCCC GGGTTCAAGT GATTCTCCTG	900
CCTCAGCCNC CCAAGTAGNT GGGACTACAG GGGTGCGCCA CCACGCCTGG GATAATTTTG	960
GGNTTTTTTAG TAGAGATGGC GTTTCACCAN CTTGGNGCAG GCTGGTCTTG GAACTCCTGA	1020
NATCATGATC TGCCTGCCTT AGCCTCCCCA AAGTGCTGGG ATTNCAGGGG TGAGCCACTG	1080
TTCCTGGGCC TC	1092

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGCAGTGAG CCGAGATCAT GCTGCTGTAC TCCAGCCTGG GCCACAGAGC CAAACTCCAT	60
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CTCCCAAAAA	AAAAAATAT	TAATTAATAT	GATNAAATGA	TGCCTATCTC	AGAATTCTTG	120
TAAGGATTTT	CTAGKACAAG	TGCTGGGTAT	AAACTATANA	TTCRATAGAT	GNCGATTATT	180
ACTTAYTATT	GTTATTGATA	AATAACAGCA	GCATCTACAG	TTAAGACTCC	AGAGTCAGTC	240
ACATAGAATC	TGGNACTCCT	ATTGTAGNAA	ACCCCNMMAG	AAAGAAAACA	CAGCTGAAGC	300
CTAATTTTGT	ATATCATTTA	CTGACTTCTC	TCATTCATTG	TGGGGTTGAG	TAGGGCAGTG	360
ATATTTTTGA	ATTGTGAAAT	CATANCAAAG	AGTGACCAAC	TTTTTAATAT	TTGTAACCTT	420
TCCTTTTTAG	GGGGAGTAAA	ACTTGGATTG	GGAGATTTCA	TTTTCTACAG	TGTTCTGGTT	480
GGTAAAGCCT	CAGCAACAGC	CAGTGGAGAC	TGGAACACAA	CCATAGCCTG	TTTCGTAGCC	540
ATATTAATTG	TMMSTATACA	CTAATAAGAA	TGTGTCAGAG	CTCTTAATGT	CMAAACTTTG	600
ATTACACAGT	CCCTTTAAGG	CAGTTCTGTT	TTAACCCAG	GTGGGTAAA	TATTCCAGCT	660
ATCTGAGGAG	CTTTTNGATA	ATTGGACCTC	ACCTTAGTAG	TTCTCTACCC	TGGCCACACA	720
TTAGAATCAC	TTGGGAGCTT	TTAAACTGT	AAGCTCTGCC	CTGAGATATT	CTTACTCAAT	780
TTAATTGTGT	AGTTTTTAAA	ATTCCCCAGG	AAATTCGGT	ATTTCTGTTT	AGGAACCGCT	840
GCCTCAAGCC	TAGCAGCACA	GATATGTAGG	AAATTAGCTC	TGTAAGGTTG	GTCTTACAGG	900
GATAAACAGA	TCCTTCCTTA	GTCCCTGGAC	TTAATCACTG	AGAGTTTGGG	TGGTGGTTTT	960
GGATTTAATG	ACACAACCTG	TAGCATGCAG	TGTTACTTAA	GAC		1003

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGATCCCTCC	CCTTTTTAGA	CCATACAAGG	TAACTCCGG	ACGTTGCCAT	GGCATCTGTA	60
AACTGTCATG	GTGTTGGCGG	GGAGTGTCTT	TTAGCATGCT	AATGTATTAT	AATTAGCGTA	120
TAGTGAGCAG	TGAGGATAAC	CAGAGGTCAC	TCTCCTCACC	ATCTTGTTTT	TGGTGGGTTT	180
TGGCCAGCTT	CTTTATTGCA	ACCAGTTTTA	TCAGCAAGAT	CTTTATGAGC	TGTATCTTGT	240
GCTGACTTCC	TATCTCATCC	CGNAACTAAG	AGTACCTAAC	CTCCTGCAAA	TTGMAGNCCA	300
GNAGGTCTTG	GNCTTATTTN	ACCCAGCCCC	TATTCAARAT	AGAGTNGYTC	TTGGNCCAAA	360
CGCCYCTGAC	ACAAGGATTT	TAAAGTCTTA	TTAATTAAGG	TAAGATAGKT	CCTTGSATAT	420
GTGGTCTGAA	ATCACAGAAA	GCTGAATTTG	GAAAAAGGTG	CTTGGASCTG	CAGCCAGTAA	480

ACAAGTTTTTC ATGCAGGTGT CAGTATTTAA GGTACATCTC AAAGGATAAG TACAATTGTG	540
TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG	600
AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTTA AACTGCATAC TTCCTGTACA	660
TTGTTTTTTC TTGCTTCAGG TTTTGTAGAAC TCATAGTGAC GGGTCTGTTG TTAATCCCAG	720
GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTTAC TGAAAATGTT TTTCTTGTGC	780
TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCCT	840
GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTTCTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT	1200
CATGTTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG	1260
ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCTTTTNC TNACTTKGGN GGATTAAATT	1380
CCTGTCATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTTCC TTTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTTG GGACAAGGGA GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCCNGCT GNTGTGTNCT NCCCCACTG ANTAGGGTTA	1620
GACTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTTAA AGAGAATNAT GGGGTGAATG	1680
CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNCGTATAAA	AGACCAACAT	TGCCANCNAC	AACCACAGGC	AAGATCTTCT	CCTACCTTCC	60
CCCNNGGTGT	AATACCAAGT	ATTCNCCAAT	TTGTGATAAA	CTTTCATTGG	AAAGTGACCA	120
CCCTCCTTGG	TTAATACATT	GTCTGTGCCT	GCTTTCACAC	TACAGTAGCA	CAGTTGAGTG	180
TTTGCCCTGG	AGACCATATG	ACCCATAGAG	CTTAAAATAT	TCAGTCTGGC	TTTTTACAGA	240
GATGTTTCTG	ACTTTGTTAA	TAGAAAATCA	ACCCAAGTGG	TTTAAATAAT	GCACATACTT	300
TCTCTCTCAT	AGAGTAGTGC	AGAGGTAGNC	AGTCCAGATT	AGTASGGTGG	CTTCACGTTC	360
ATCCAAGGAC	TCAATCTCCT	TCTTTCTTCT	TTAGCTTCTA	ACCTCTAGCT	TACTTCAGGG	420
TCCAGGCTGG	AGCCCTASCC	TTCATTTCTG	ACAGTAGGAA	GGAGTAGGGG	AGAAAAGAAC	480
ATAGGACATG	TCAGCAGAAT	TCTCTCCTTA	GAAGTTCCAT	ACACAACACA	TCTCCCTAGA	540
AGTCATTGCC	CTTACTTGTT	CTCATAGCCA	TCCTAAATAT	AAGGGAGTCA	GAAGTAAAGT	600
CTKKNTGGCT	GGGAATATTG	GCACCTGGAA	TAAAAATGTT	TTTCTGTGAA	TGAGAAACAA	660
GGGGAAGATG	GATATGTGAC	ATTATCTTAA	GACAACTCCA	GTTGCAATTA	CTCTGCAGAT	720
GAGAGGCACT	AATTATAAGC	CATATTACCT	TTCTTCTGAC	AACCACTTGT	CAGCCCNCGT	780
GGTTTCTGTG	GCAGAATCTG	GTTCYATAMC	AAGTTCCTAA	TAANCTGTAS	CCNAAAAAAT	840
TTGATGAGGT	ATTATAATTA	TTTCAATATA	AAGCACCAC	TAGATGGAGC	CAGTGTCTGC	900
TTCACATGTT	AAGTCCTTCT	TTCCATATGT	TAGACATTTT	CTTTGAAGCA	ATTTTAGAGT	960
GTAGCTGTTT	TTCTCAGGTT	AAAAATTCTT	AGCTAGGATT	GGTGAGTTGG	GGAAAAGTGA	1020
CTTATAAGAT	NCGAATTGAA	TTAAGAAAAA	GAAAATTCTG	TGTTGGAGGT	GGTAATGTGG	1080
KTGGTGATCT	YCATTAAACAC	TGANCTAGGG	CTTTKGKGTT	TGKTTTATTG	TAGAATCTAT	1140
ACCCCATTCA	NAGAAGATAC	CGAGACTGTG	GGCCAGAGAG	CCCTGCACTC	AATTCTGAAT	1200
GCTGCCATCA	TGATCAGNGT	CATTGTWGTG	ATGACTANNC	TCCTGGTGGT	TCWGTATAAA	1260
TACAGGTGCT	ATAAGGTGAG	CATGAGACAC	AGATCTTTGN	TTCCACCCT	GTTCTTCTTA	1320
TGGTTGGGTA	TTCTTGTCAC	AGTAACTTAA	CTGATCTAGG	AAAGAAAAAA	TGTTTTGTCT	1380
TCTAGAGATA	AGTTAATTTT	TAGTTTTCTT	CCTCCTCACT	GTGGAACATT	CAAAAAATAC	1440
AAAAAGGAAG	CCAGGTGCAT	GTGTAATGCC	AGGCTCAGAG	GCTGAGGCAG	GAGGATCGCT	1500
TGGGCCCAGG	AGTTCACAAG	CAGCTTGGGC	AACGTAGCAA	GACCCTGCCT	CTATTAAAGA	1560
AAACAAAAAA	CAAATATTGG	AAGTATTTTA	TATGCATGGA	ATCTATATGT	CATGAAAAAA	1620
TTAGTGTAAG	ATATATATAT	TATGATTAGN	TATCAAGATT	TAGTGATAAT	TTATGTTATT	1680

TTGGGATTTC AATGCCTTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAAA	1740
AGTTGTAACT GAAAAATAAA CATTTCATA TAATAGCACA ATCTAAGTGG GTTTTTGNTT	1800
GTTTGTTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT	1860
GGCACGATTT TGGCTCACTG CAG	1883

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGTTTGACA ATTTCTCCGT TCCACCCTTG ATTAAATAAG GTAGTATTCA TTTTTTAAGT	60
TTTAGCTTTT GGATATATGT GTAAGTGTGG TATGCTGTCT AATGAATTAA GACAATTGGT	120
NCTKTCTTTA CCCMACANCT GGACMAAGAG CAGGCAAGAT NCAANAATCA AGTGACCCAG	180
NCAAACCAGA CACATTTTCT GCTCTCAGCT AGCTTGCCAC CTAGAAAGAC TGGTTGTCNA	240
AGTTGGAGTC CAAGAATCGC GGAGGATGTT TAAATGCAG TTTCTCAGGT TCTCNCCACC	300
CACCAGAAGT TTTGATTCAT TGAGTGGTGG GAGAGGGCAG AGATATTTGC GATTTTAACA	360
GCATTCTCTT GATTGTGATG CAGCTGGTTC SCAAATAGGT ACCCTAAAGA AATGACAGGT	420
GTAAATTTA GGATGGCCAT CGCTTGATG CCGGGAGAAG CACACGCTGG GCCCAATTTA	480
TATAGGGGCT TTCGTCTCA GCTCGAGCAR CCTCAGAACC CCGACAACCY ACGCCAGCKC	540
TCTGGGCGGA TTCCRTCAGK TGGGGAAGSC CAGGTGGAGC TCTGGKTTCT CCCCAGCAATC	600
GTTTCTCCAG GCCGGAGGCC CCGCCCCCTT CCTCCTGGCT CCTCCCCTCC TCCGTGGGCC	660
GNCCGCCAAC GACGCCAGAG CCGGAAATGA CGACAACGGT GAGGGTTCTC GGGCGGGGCC	720
TGGGACAGGC AGCTCCGGGG TCCNCGNNWT NACATCGGAA ACAAACAGC GGCTGGTCTG	780
GAAGGAACCT GAKCTACGAC CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATGTGCGTG	840
ATGGGGAGTC CGGGCAAGCC AGGAAGGCAC CGCGGACATG GGCGGCCGCG GGCAGGGNCC	900
GGNCCTTTGT GGCCGCCCGG GCCGCGAAGC CGGTGTCCTA AAAGATGAGG GGCGGGGCGC	960
GGCCGGTTGG GGCTGGGGAA CCCCCTGTGG GAAACCAGGA GGGGCGGCCC GTTTCTCGGG	1020

CTTCGGGCGC GGCCGGGTGG AGAGAGATTC CGGGGAGCCT TGGTCCGGAA ATGCTGTTTG	1080
CTCGAAGACG TCTCAGGGCG CAGGTGCCTT GGGCCGGGAT TAGTAGCCGT CTGAACTGGA	1140
GTGGAGTAGG AGAAAGAGGA AGCGTCTTGG GCTGGGTCTG CTTGAGCAAC TGGTGAAACT	1200
CCGCGCCTCA CGCCCCGGGT GTGTCCTTGT CCAGGGGCGA CGAGCATTCT GGGCGAAGTC	1260
CGCACGCCTC TTGTTCGAGG CGGAAGACGG GGTCTTGATG CTTTCTCCTT GGTCGGGACT	1320
GTCTCGAGGC ATGCATGTCC AGTGACTCTT GTGTTTGCTG CTGCTTCCCT CTCAGATTCT	1380
TCTCACCGTT GTGGTCAGCT CTGCTTTAGG CATATTAATC CATAGTGGAG GCTGGGATGG	1440
GTGAGAGAAT TGAGGTGACT TTTCCATAAT TCAGGTGAGA TGTGATTAGA GTYCGGATCC	1500
TNCGGTGGTG GCAGAGGCTT ACCAAGAAAC ACTAACGGGA CATGGGAACC AATTGAGGAT	1560
CCAGGGAATA AAGTGTGAAG TTGACTAGGA GGTTTTCAGT TTAAGAACAT GGCAGAGACA	1620
TTCTCAGAAA TAAGGAAGTT AGGAAGAAAG ACCTGGTTTA GAGAGGAGGG CGAGGAAGTG	1680
GTTTGGAAGT GTCACCTTGG AAGTGCCAGC AGGTGAAAAT GCCCTGTGAA CAGGACTGGA	1740
GCTGAAAACA GGAATCAATT CCATAGATTT CCAGTTGATG TTGGAGCAGT GGAGAAGTCT	1800
AANCTAAGGA AGGGGAAGAG GAGGCCAAGC CAAACACTTA GGAACACTTN CNACGAGGGG	1860
GTGGAAGAAG AGCAAGGAGC CAGCTGAGGA GAATGAGTGT GGTGGAGAA CCACCACAGC	1920
NCAGGGTCGC CAGANCTGAG GAAGGGGAGG GAAGCTTATC GAGKAMSGWC RACMKCGAGT	1980
TGGCAGGGAT	1990

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CTTACATTA TTACTCCTTG CCATTTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA	180
TATTTGCGGT TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA	240

CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCC GGCTGG ACTTTTGGAG	300
GTTCCCTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA	360
GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA	420
GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCATCAGC	480
AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGACTACCGT	540
TACCAAGAGG TTAGGTGAAG TGGTTTAAAC CAAACGGAAC TCTTCATCTT AAACCTACAG	600
TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTTCAG GAGGTACTGT	660
GAGGAAGAGC AGGCACCACC AGCAGAAATGG GGAATGGAGA GGTGGGCAGG GGTTCCAGCT	720
TCCCTTTGAT TTTTGG	736

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNNWGTA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACA TTCCNTTAAG GATTACTCAA GCYCCCCTTT TGSTGKNWAA TCAGANNGTC	360
ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTC CTA CTATTATTG	420
CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA	480
TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT	540
ACTAGGATTT AACTAACAAT GGATGACCTG GTGAAATCCT ATTTGAGACC TAATCTGGGA	600
GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT	660
GAAAGAMMGG TTTGWNTCTG NTTAWTGTA TCTATGRAAG TGTTTTTWAT MACAGTATAA	720
TTGTMGTMAC AAAGTTCTGT TTTTCTTTCC CTTTNCAGAA CCTCAAGAGG CTTTGTTTTC	780
TGTGAAACAG TATTTCTATA CAGNTGCTCC AATGACAGAG TNACCTGCAC CGTTGTCCTA	840
CTTCCAGAAT GCACAGATGT CTGAGGACAA CCACCTGAGC AATACTGTAC GTAGCCAGGT	900

ACAGCGTCAG TYTCTNAAAC TGCCTYYGNC AGACTGGATT CACTTATCAT CTCCCCTCAC	960
CTCTGAGAAA TGCTGAGGGG GSTAGGNAGG GCTTTCTCTA CTTNACCACA TTTNATAATT	1020
ATTTTTGGGT GACCTTCAGC TGATCGCTGG GAGGGACACA GGGCTTNTTT AACACATAGG	1080
GTGTTGGATA CAGNCCCTCC CTAATTCACA TTTCANC	1117

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTTA	120
TNTTGTTTAT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTTATT TCATATTCAT	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTTCCT TCGTTAATTC	240
CTCCCTACCA CCCATTTACA AGTTTAGCCC ATACATTTTA TTAGATGTCT TTTATGTTTT	300
TCTTTTNCTA GATTTAGTGG CTGTTTNGTG TCCGAAAGGT CCACTTCGTA TGCTGGTTGA	360
AACAGCTCAG GAGAGAAATG AAACGCTTTT TCCAGCTCTC ATTTACTCCT GTAAGTATTT	420
GGAGAATGAT ATTGAATTAG TAATCAGNGT AGAATTTATC GGGAATTGA AGANATGTNA	480
CTATGGCAAT TTCANGGNAC TTGTCTCATC TTAAATGANA GNATCCCTGG ACTCCTGNAG	540

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCCCGTCNAT GCATACTTTG TGTGTCCAGT GCTTACCTGG AATCCNGTCT TTCCCAACAG	60
CAACAATGGT GTGGTTGGTG AATATGGCAG AAGGAGACCC GGAAGCTCAA AGGAGAGTAT	120
CCAAAAATTC CAAGTATAAT GCAGAAAGTA GGTAACYYYY NTTAGATAMN ATCTTGATTT	180
TNCAGGGTCA CTGTTATAAG CTAACAGTAT AGNAATGTTT TTATCGTCTT TCTNKGGNCA	240
TAGACTCCTN KGAGAATCTC TTGAGAACTA TGATAATGCC CAGTAAATAC NCAGATAAGT	300
ATTTAAGGAG TNCAGATACT CAAANCCCAA CAATACNGTC AAAGCATCCT AGGTTAAGAC	360
AMCNCCCATT AAATACAGAA TACCAGCATG GAAAGGTTCA GGCTGAGGTT ATGATTGGGT	420
TTGGGTTTTG GGNNNGTTTT TTATAAGTCA TGATTTTAAA AAGAAAAAAT AAACCTCTCTC	480
CAAACATGTA AAAGTAAGAA TCTCCTAAA	509

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 823 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CAGGAGTGGA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCNG GGACATAGTG	60
GTACACANCT GTAATGCTCA NCACTKATGG GGAGTACTGA AGGNGGNSGG ATCACTTGNG	120
GGTCNGGAAT NTGAGANCAG CCTGGGCAAN ATGGCGAAAC CCTGTCTCTA CTAAAAATAG	180
CCANAAWNWA GCCTAGCGTG GTGGCGCRCA CGCGTGGTTC CACCTACTCA GGAGGCNTAA	240
GCACGAGNAN TNCTTGAACC CAGGAGGCAG AGGNTGTGGT GARCTGAGAT CGTGCCACTG	300
CACTCCAGTC TGGGCGACMA AGTGAGACCC TGTCTCCNNN AAGAAAAAAA AAATCTGTAC	360
TTTTTAAGGG TTGTGGGACC TGTTAATTAT ATTGAAATGC TTCTYTTCTA GGTCATCCAT	420
GCCTGGCTTA TTATATCATC TCTATTGTTG CTGCTCTTTT TTACATTCAT TTAATTGGGG	480
TAAGTTGTGA AATTTGGGGT CTGTCTTTCA GAATTAACTA CCTNNGTGCT GTGTAGCTAT	540
CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTTAATTGT NTCCACATAT	600
AGGTCATACT TGGTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG	660
CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACTTAAGA CTACAGTTAA TTCTAAGCCT	720

TTGGGGAAGG ATTATATAGC CTTCTAGTAG GAAGTCTTGT GCNATCAGAA TGTTTNTAAA	780
GAAAGGGTNT CAAGGAATNG TATAAANACC AAAAATAATT GAT	823

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACCAAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTANAGGGAA	180
GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240
TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTTGG TGGAAATTAT	300
TGTACATCTT TTAATACTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC	480
CCTCATGNCC CTGKTGTTTA TCAAGTACCT CCCTGAATGG ACTGNGTGCC TCATCTTGGC	540
TGTGATTTC A GTATATGGTA AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC	600
ACTGGAGTGT TTTCTTTCCT CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAATT AGCTATAGTA ACTTTTTTCAT TTGAAGATTT	720
CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG	780
ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Tyr Thr Pro Phe
1

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ser Thr Pro Glu
1

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTCACTGA GGACACACC

19

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TGTAGAGCAC CACCAAGA

18

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCATGGTGTG CATCCACT

18

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GGACCACTCT GGGAGGTA

18

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AAACTTGGAT TGGGAGAT

18

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn	Asp	Asn	Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Lys	Asp	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu
1			5				10						15	

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ser His Leu Gly Pro His Arg Ser Thr Pro Glu Ser Arg Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CAGAGGATGG AGAGAATAC

19

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCTCCCCAA AACTGTCAT

19

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCCCTAGTGT TCATCAAGTA

20

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AAAGCGGGAG CCAAAGTC

18

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TCACAGAAGA TACCGAGACT

20

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CCCAACCATA AGAAGAACAG

20

- (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

TCTGTACTTT TTAAGGGTTG TG

22

- (2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ACTTCAGAGT AATTCATCAN CA

22

- (2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GACTCCAGCA GGCATATCT

19

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GATGAGACAA GTNCCNTGAA

20

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TTAGTGGCTG TTTNGTGTCC

20

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

164+

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CACCCATTTA CAAGTTTAGC

20

C1
cont